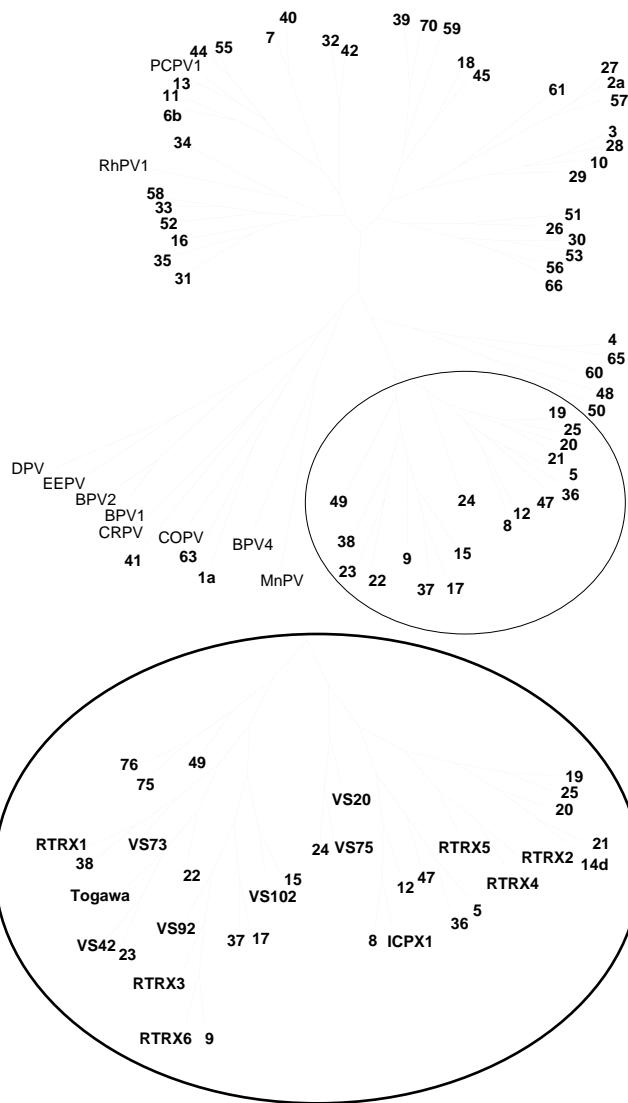


# Group B1 Sequences

|               |              |
|---------------|--------------|
| HPV5          | HPV8         |
| HPV9          | HPV12        |
| HPV14d        | HPV15        |
| HPV17         | HPV19        |
| HPV20         | HPV21        |
| HPV22         | HPV23        |
| HPV24         | HPV25        |
| HPV36         | HPV37        |
| HPV38         | HPV47        |
| HPV49         | HPV75 (VS40) |
| HPV76 (CR148) | HPVICPX1     |
| HPVRTRX1      | HPVRTRX2     |
| HPVRTRX3      | HPVRTRX4     |
| HPVRTRX5      | HPVRTRX6     |
| HPVVS20       | HPVVS42      |
| HPVVS73       | HPVVS75      |
| HPVVS92       | HPVVS102     |
| HPVTogawa     |              |



## INTRODUCTION

Group B1 viruses composed the old group H and are primarily associated with the multifactorial disease Epidermodysplasia Verruciformis (EV). Recent work suggests they are also commonly associated with immunosuppressed renal transplant recipients [1,2]. Several isolates which appear to constitute new types have been found in skin lesions of renal transplant patients [5,6]. Association of EV-related HPV types with squamous cell carcinomas (SCC) of the skin, and with SCCs of the esophagus has recently been suggested [3,4,5,7,27]. One potential new type was isolated from an immunocompetent patient [5].

Patients with EV tend to have depressed cell-mediated immunity [8]. In roughly one-third of EV-associated HPV infection, the sun-exposed flat wart-like or macular lesions transform into malignant squamous cell carcinomas [9]. Benign wart scrapings tend to be multiply-infected, with as many as six different viral types. However, in contrast, EV carcinomas tend to harbor only a few types, specifically HPV-5 and HPV-8, and less frequently HPV-14, HPV-17, HPV-20 and HPV-47 [9,10]. These types are rarely detected in lesions afflicting the general population. A key to host restriction of these viruses may be in part due to the unusual organization of the LCR in these viruses. The LCR of these viruses is short compared to the viruses in other groups; most of the types in this group also contain two EV-specific regulatory regions: M33 and M29, both shown to be involved in protein binding [10,11,12]. Study of variants of HPV5 and HPV8 has revealed a higher level of sequence diversity within these types [13,14,15] than has been observed in primarily mucosal types such as HPVs 6, 11, 16 and 18 [16,17,18], suggesting that the EV-related types may accumulate mutations at a higher rate. One possible explanation for this is that the cutaneous tropism of the EV types could lead to additional mutations through UV-induced DNA damage; however, sequencing of variants of primarily cutaneous HPV2 show levels of variability comparable with that seen in the mucosal types [19].

This group forms two major branches based on phylogenetic analysis, each of which can be subdivided into two minor branches. These clusters have been designated as a<sub>1</sub>, a<sub>2</sub>, b<sub>1</sub>, and b<sub>2</sub>.

This phylogenetic classification is compatible with other classifications based on hybridization [21], transforming activity of the E6 gene [20], and conservation of the M33 and M29 regions and E2 binding sites in the LCR [11]. In addition, HPV-24, HPV-49, and several of the new sequences seem to form isolated branches, which may be related with their detection in immunosuppressed, non-EV patients.

**Cluster a<sub>1</sub>** consists of HPV-5, HPV-8, HPV-12, HPV-36 and HPV-47; the available sequence of HPVICPX1 suggests that it too is a member of this cluster. Both HPV-5 and HPV-8 are associated with macular lesions which frequently progress to malignancy [22,23,24]. Yabe et al. studied the characteristics of HPV-5 in lesions of differing severity. In a primary carcinoma, HPV-5 was present in an episomal state with a 40% subgenomic segment amplified. In the metastatic tumor, only the 40% subgenomic region was present, but integrated into the host genome [24]. The segment was determined to be the entire sequences of E6, E7, and the noncoding region and portions of E1 and L1, with no mutations present [25]. In addition, amplifications of the LCR have been reported in HPV-5 associated carcinomas [26]. HPV-5 and HPV-8 have also been found in significant numbers in squamous cell carcinomas of renal allograft patients. Barr et al. detected either HPV-5 or HPV-8 in nearly 60% of the cases surveyed in Scotland [27]. HPV-47 is primarily associated with benign lesions; however, it has also been detected in cases of malignancy [20]. HPV-12 induces benign macular and flat wart-like lesions [28]. HPV36 was isolated from two patients with actinic keratosis. HPVICPX1 was isolated from an immunocompetent patient [5]; other information is not currently available.

**Cluster a<sub>2</sub>** consists of HPV-14, HPV-19, HPV-20, HPV-21 and HPV-25. HPV types forming this cluster produce benign macular or flat wart-like lesions and malignant lesions in isolated cases. Both HPV-19 and HPV-25 induce macular lesions, which are benign in character [21,20,29]. HPV-14, HPV-20 and HPV-21 induce flat-wartlike lesions; HPV-20 and HPV-14 have been detected in carcinomas [20,29].

**Cluster b<sub>1</sub>** includes of HPV-9, HPV-15, HPV-17, and HPV-37; available sequence indicates that

HPVRTRX3, HPVVS92 and HPVVS102 are also members of this cluster [5,6]. HPV-15 was isolated from a benign flat wart-like lesion [29]. HPV-17 was isolated from benign macules and subsequently from squamous cell carcinomas and the malignant melanoma of an immunosuppressed patient [29,30]. HPV 9 DNA induces both macular and flat wart-like lesions, however it has also been identified in a keratoacanthoma [28,31]; HPV-37 was found in the same keratoacanthoma. HPVRTRX3, HPVVS92, and HPVVS102 were isolated from a squamous cell carcinoma, skin wart, and dysplastic wart respectively in renal transplant patients [5,6]. Also possibly belonging to this cluster is HPVRTRX6, although its position in phylogenetic trees is rather unstable. HPVRTRX6 was isolated from an SCC in one renal transplant patient [5].

**Cluster b<sub>2</sub>** includes HPV-22, HPV-23, and HPV-38; available sequence indicates that HPVRTRX1, the Togawa isolate, HPVVS42 and HPVVS73 are also members of this cluster. HPV-22 and HPV-23 were isolated from macules of EV patients [29]. HPV-38 was isolated, along with HPV17a, from a superficial spreading melanoma in an immunocompromised patient [31]. The Togawa isolate was found in multiple SCCs of the esophagus in nonimmunocompromised patients [7]. HPVRTRX1, HPVVS42 and HPVVS73 were isolated from an SCC, a verrucous biopsy and a skin wart biopsy in renal transplant patients [5,6].

**Isolated types** Several EV-related types or potential new types seem to be relatively unrelated to the clusters defined above, and, for the most part, to each other. HPV-49 was isolated from the flat warts of a Polish renal transplant patient. Favre et al. screened benign and malignant lesions from the general population, EV patients and transplant patients for the presence of HPV-49. In the survey, HPV-49 was not detected in any of the patients with EV but was detected in two additional cases of flat warts in renal transplant patients [32]. Related to HPV49 are HPV-75 (VS40) and HPV-76 (CR148), from a dysplastic wart biopsy and a skin wart biopsy, respectively, from renal transplant patients [6].

HPV-24 was isolated from macules in an EV patient [29]. HPVVS75 and HPVVS20 appear to be relatively closely related to HPV24, and were isolated from skin wart biopsies of renal transplant patients [6].

HPVRTRX2, HPVRTRX4, and HPVRTRX5 appear to form their own cluster, and were all isolated from cutaneous SCCs of renal transplant patients [5]. HPVRTRX2 and HPVRTRX5 were each isolated from one SCC in each of two patients, and HPVRTRX4 was isolated once, out of 53 SCCs from 26 renal transplant patients.

HPV-5, HPV36 and HPV-47 are close enough to each other to be considered “close types”— sequences that qualify to be distinct types under the criterion of ten percent dissimilarity at the nucleotide level, but between which most of these changes are “silent”, causing no difference at the amino acid level (Part III). Also qualifying as close types are HPV-19 and HPV-25, and HPV-14d, HPV-20f and HPV-21.

### What's new?

The complete genomes of HPV-20 and HPV-21 have been released since last year's publication and are given on the following pages. In addition new complete genomes for HPV types 22, 23, 24, 36, 37, and 38 are available. The newly designated types HPV-75 and HPV-76 are represented here by the sequences of a fragment of L1. Sequences of fragments of L1 from fourteen potential new types, drawn from renal transplant patients, immunocompetent patients and SCC of the esophagus, are included as well. Please refer to *Human Papillomaviruses 1994* pp. I-H-4 et seq., for the sequences of other members of this group.

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**HPV20**

LOCUS HPV20 7757 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 20, complete genome.  
ACCESSION U31778  
KEYWORDS .  
SOURCE Human papillomavirus type 20.  
REFERENCE 1 (bases 1 to 7757)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kremsdorf,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A.,  
Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G.  
TITLE Molecular cloning and characterization of the genomes of nine newly  
recognized human papillomavirus types associated with  
epidermodysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1013-1018 (1984)  
REFERENCE 3 (sites)  
AUTHORS Gassenmaier,A., Lammel,M. and Pfister,H.  
TITLE Molecular cloning and characterization of the DNAs of human  
papillomaviruses 19, 20, and 25 from a patient with epidermo-  
dysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1019-1023 (1984)  
REFERENCE 4 (sites)  
AUTHORS Kiyono,T., Hiraiwa,A. and Ishibashi,M.  
TITLE Differences in transforming activity and coded amino acid sequence  
among E6 genes of several papillomaviruses associated with  
epidermodysplasia verruciformis  
JOURNAL Virology 186 (2), 628-639 (1992)  
MEDLINE 92124737  
REFERENCE 5 (bases 1 to 7757)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Laboratory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV20 was originally isolated from skin warts of epidermodysplasia  
verruciformis (EV) patients [2,3]. It has additionally been  
detected in a squamous cell carcinoma from another EV patient,  
although the association is not frequent. Hybridization assays  
and phylogenetic reconstructions based on DNA sequences indicate  
that HPV20 is most closely related to HPV21 and HPV14, and then to  
HPV19 and HPV25. This grouping agrees with assays of the degree of  
transforming activity of the E6 protein (these related HPV types  
had relatively low transforming activity as compared to HPVs 5, 8,  
and 47), and clustering of similarity of amino acids in the second  
zinc finger domain of E6 [4]. The E6 gene of HPVs 14, 21, and 25  
can enhance the induction of anchorage independent growth of 3Y1  
cells by the HPV16 E7 gene, although again less effectively than  
that of HPVs 5, 8, and 47. HPV20 was cloned via *AvaI* restriction.  
But contrary to the assumption that type 20 had only one *AvaI* site  
(Kremsdorf et al., 1984) the sequence analysis of the clone showed  
the presence of two additional *AvaI* fragments of 16 and 176 nt,  
respectively, at the cloning site (position 1158 in the final  
sequence) in opposite orientation relative to the large *AvaI*  
fragment containing the major part of the viral genome. The segment  
between the *AvaI* sites at position 1142 and 1334 is inverted in the  
*pBR322* clone. This inversion leads to disrupted E7 and E1 ORFs in  
the clone. The sequence has been fixed to yield colinearity with



HPV20

2761 tcagcaagcg tttcaatgct ctgcaagatc agctaatacg catttaTGAg tctgcaccag  
-< E1 end  
2821 acactcttga gtcgcaaatt gaggcactggc aaaccctgcg aaaagaagct gtgctactat  
2881 attttgcgtat gcaacatggt atcagcaggg ttggatatca acctgtgcct gtattagctg  
2941 tgtcagaagc caaaagctaa caggctatag gaatggatt aaggttacaa tcattgcaa  
3001 aatctgaata tggaagtgaa ccatggctt ttgttagatgc aagtgcagag acatttagaa  
3061 gcccggcaga aaatcactt aaaaaaggc cgatttcagt agaggtcata tatgacaaga  
3121 ataaaagacaa tgccaatgct tataccatgt ggagatttg ttattacca gatgatgacg  
3181 acaagtggca caaaaagtgc agtgggtt accaaacagg catatattt atgcaaggaa  
3241 catttagaca ctactatgtt ttgtttgcgt atgatgcgag tagatatagt acaactggac  
3301 aatgggaagT GAaaggtaat aaggaaactg tggttgcgtcc tgtcaccagc tccacccccc  
E4 orf start ->  
NH<sub>2</sub> terminus unknown  
3361 ccgactcacc aggaggacaa gcagactcaa acgcctcctc ccagaccccc gccaccacca  
3421 ctgactccac gaccagacag tcgcccagaa aacagtccaca acaaaccaac acaaaggaa  
3481 gaaggtacgg acggagacct tcaggtagga caaggcgaac aacccaaacg cgccagggc  
3541 gacggtccag gtcaaagtcc aagtccaaatg ccaggtcgcg gtcgaggctg cggcACCGGT  
E2 binding ->  
3601 CTCGGTctcg gtctcggtct gaatcgccgc gcccgggtc tcggtaccga tcacgatccg  
3661 gatccagagg gagagtgcgcc cttccgcgcca ttaccaccac caccacaacc accaccagac  
3721 gggcaggtgg agggtcaccc acctccaccc cttccaccc ctcacaacgg tcgacagc  
3781 tgcggggagg gggccgtggg gggagcagac aaagagcaag gggaaaggcga tcatcatcca  
3841 cctcccccac cccctcaaaa cgttcacgg gggagtcaga gtctgttagg caacatggca  
3901 tctctccccc tgacgtggga acagcagttt acacagttt ttcaagacat acaggaagac  
3961 ttggaagatt actggatgaa gctctcgatc ccccaatGAt tttagtttagg ggagagccta  
-< E4 end  
4021 atacgcttaa gtgcttcgc aatagggcca aacaaagata tacagggctg tataagtctt  
4081 tttagcacggc ctggcgtgg gtggctggag atggcacggg gcgcttaggc aggtccagaa  
4141 tgctcatttag ctttatatcc ttcaatgtt gaaaagattt tgatgagact gtgaaatatc  
4201 cgaaggggggt tgaccggcgtc ttgggttcat ttgacagctt aTAGcaacct aaccccttcaa  
-< E2 end  
4261 ccactgcatg ctactaacac actaacat tttttttt attAAAtattt tttatTTGCT  
L2 orf start ->  
4321 ATGgcgcgcg ctaagcgagt caagcggac tctgctacta acatatacag aacctgcaaa  
L2 cds ->  
4381 caagcaggtt cttgtccctcc tgatgttata AATAAAAtgg aaagcacaac tattgctgat  
signal ->  
4441 aaaatttgc agtatggtag tgctgggtt tttttgggg gattaggcat aagcactgaa  
4501 aaaggtacag gaggaccac agtttatgtg ctttggggag aaggcccac ggtgcgtt  
4561 ggtgtacac ctacagtcat acgACCTGCT TTGGTcccaac acaccatcg cccctccgat  
E2 binding ->  
4621 attatacctg tggacacccctt aatccgggt gaggccttcta ccttttctat tggccactt  
4681 acagaatcca caggaccaga tcttttaccc ggtgaagtgg aaactattgc agaaatacat  
4741 ccaggccccctt caaggccacc aactgataca ccagttacat ctactaccag tgggtcttagt  
4801 gcagttctag aggttagcacc agaaccacaa cctccagtc gttgtcagat cagccgcacc  
4861 cagttatcata accccatcatt tcaaataata actgaatcaa caccaacatt gggggaaagc  
4921 tcatttagcggtt atcataatgtt agtgacatct ggttctgggg gccaagcaat tggggggatg  
4981 acaccccttcaatggatgtt tcaggatttccatcaatggat attcatttga aatagaagac  
5041 ccaaccccttcaatggatgtt tcaggatttccatcaatggatgtt gttcaggcgtt  
5101 agaggaggcc ttactaacag aagattgtt caacaatgc ctgttagacaa tccattatattt  
5161 ttgacacaaatccctt cttcttagatt ggtccgggtt cagttgtata accccgttt tgagggaa  
5221 gttactcaaa tattttaaaca agatggatgtt acctttatgtt agcccccaga cagagactt  
5281 ttggatgttc agagtttagg caggcctcaa tactcagaaa ctcctgcagg ttatgtgcgg  
5341 gtcagccgtg caggtaacg aaggactatc agaactcggtt ctggagcaca aatagggtct  
5401 caagtgcact tttatagaga tctcagtagt attgatacag aagatccat tgaactgcac  
5461 ttgttgggtc agcattctgg cgtatgcactt attgtccaaatg gtcaggataga aagcacttt  
5521 gttgatataca atgttagatgaa aaacccactt tcagaaatca gtgcattttc tgatgattt  
5581 cttttagatg aagctaatgaa agacttttagt ggctctcgtt tagtgttagg gggaaaggcgtt  
5641 tctacatctt catacaactgt tcctcaatgtt gaaactacta gatctgcactt ttactatgtt

5701 caagatacaa aggggtatta tgttagcatat cctgaagata gagatgttag taaggacatt  
 5761 atttattccta atccagattt accagtggtc attattcaca catatgacac aagtggagat  
 5821 ttttatttac atccaagtct tactaaaaga ttaaaaagaa aaagggaaata tttgTAActt  
<- L2 end  
L1 orf start ->  
 5881 tttctttgc agATGgcagt ttggcaagca gctagtggta aggtgtacct tccaccatct  
L1 cds ->  
 5941 acaccagttt ccagggtcca aagtacggat gaatatgtgc aaaggactaa catatactat  
 6001 catgcataca gtgatcgcc actaactgtt ggtcatccat attttaatat atatgacatc  
 6061 caaggcacta agataaaaat ccctaagggtt tctggaaatc agcacagagt gtttaggtta  
 6121 aaactaccag atcccaacag atttgatttgc gcagatatgt ctgtgtataa cccagataaa  
 6181 gaaagattgg tctggggctg tagaggtata gaaataggtt gaggacagcc attaggcggtt  
 6241 ggaagtgttag gtcattccatt attaataaaa ctttgtgaca cagaaaaaccc taattcataat  
 6301 aaagggaaatt caactgtatgta tagacaaaat gtatcttttgc accctaaaca actacaaatg  
 6361 tttataatag gctgtgcccc atgtttagga gaacattggg acagggtttt accatgtgca  
 6421 gacgacgttc caaaacccagg ttcattccctt ccaatagaat taaaaaaatac agcaatacaa  
 6481 gatggcgata tggcagatattt aggatatggc aacctaattt taaaaggcatt acaagaaaac  
 6541 agagcagatg taagtttggg tattgttaat gagacctgtt aatatccaga cttttttaaa  
 6601 atgcagaatg atgttatgg agattcctgc tttttttatg ctcggcggga acaatgttt  
 6661 gctagacact tttttgtac tggggggcaaa acaggagatg atatacctgc aggacaaaatt  
 6721 gatgaaggta gcatgaagaa tgcattctac attccacctg tgaataatca ggcacagaaac  
 6781 aaccttaggtt attcaatgtt tttcccaact gtcagtggctt catttgtgtc tagtgatgt  
 6841 caatttgttta ataggccattt tggctgcag cgccgcacagg gccacaaacaa tggcatctgc  
 6901 tggttcaatc aactattttgt tactgttagt gataatactc gaaatacaaa ttttagcata  
 6961 tcagttcattt cagaaaaacac tgatgtttctt aaaattcaaa attatgatttcc tcaaaaattt  
 7021 caagaatattt taagacacgtt agaagaatattt gaaatttcat taattttaca gctctgtaaa  
 7081 gttcccttaa cagctgaagt ttttagcttca attaatgttca tgaattcaaa tatatttagg  
 7141 gagtggcagt taggattcgt tcctgcaccc gataatccctt tccacgatac atacagatatt  
 7201 attaattctgtt cagctactatg atgtccctgtt aaaaatccctt caaaagaaaag agaagatcc  
 7261 tacaaggatc taaaacttttgc gaaatgttgc ctatcagaaa gattatccctt agaatttggat  
 7321 caatattctt taggacgcaatttcaatccctt caagcagtttca tacaacaacg gACCGTAAAC  
E2 binding ->  
 7381 GGTacaaaaaa ctgttatctt aaagtttatctt actaggggcgc tcaaaccggaaa acgcaaaacaa  
 7441 TAAaccgcAC CGTTTCGGT acAATAAAgtt caacttttac acggtttca aggaatgtt  
<- L1 end signal ->  
E2 binding ->  
 7501 atttactctg actaactaag ataccaaccg cacccgacac ataaagggtt gttgtgtgcc  
 7561 aaatgaggtt agttgtgac cagaagagat cacagccaaatc tcaggcttgc gcccacatcg  
 7621 atacactgcg tgccagatgtt ggctcaactt tcattgtccc aacacgttgc gaaacaggagg  
 7681 aaatgttcaagg ctgccaacgc ttttggctt tctttttggc acagcagaag ACCGTTAACG  
E2 binding ->  
 7741 GTaagttttt atttgc  
//

**HPV21**

LOCUS HPV21 7779 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 21, complete genome.  
ACCESSION U31779  
KEYWORDS .  
SOURCE Human papillomavirus type 21.  
REFERENCE 1 (bases 1 to 7779)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kremsdorff,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A.,  
Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G.  
TITLE Molecular cloning and characterization of the genomes of nine newly  
recognized human papillomavirus types associated with  
epidermodysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1013-1018 (1984)  
REFERENCE 3 (sites)  
AUTHORS Kiyono,T., Hiraiwa,A. and Ishibashi,M.  
TITLE Differences in transforming activity and coded amino acid sequence  
among E6 genes of several papillomaviruses associated with  
epidermodysplasia verruciformis  
JOURNAL Virology 186 (2), 628-639 (1992)  
MEDLINE 92124737  
REFERENCE 4 (bases 1 to 7779)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Laboratory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV21 was originally isolated from skin warts of an  
epidermodysplasia verruciformis (EV) patient [2]. Hybridization  
assays and phylogenetic reconstructions based on DNA sequences  
indicate that HPV21 is most closely related to HPV14 and HPV20, and  
then to HPV19 and HPV25. This grouping agrees with assays of the  
degree of transforming activity of the E6 gene (these related HPV  
types had relatively low transforming activity as compared to HPVs  
5, 8, and 47), and clustering of similarity of amino acids in the  
second zinc finger domain of E6 [3]. The E6 gene of HPVs 14, 21,  
and 25 can enhance the induction of anchorage independent growth of  
3Y1 cells by the HPV16 E7 gene, although again less effectively  
than that of HPVs 5, 8, and 47.  
BASE COUNT 2426 a 1518 c 1680 g 2155 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 acggtaagtt atgcACCGGG TGCGGTcgaa ttattactca ttgcatagtt gttgttgcca  
E2 binding ->  
61 gctaccattt aggacagcat gttttgcct gTAACgttat cgacacatac tcacaccata  
E6 orf start ->  
dinucleotide "TA" repeat region ->  
121 tatatatata tatatatata tatatatata tatatatata tattcaTATA TAcatactag  
signal ->  
181 ggaagatgcc cttagtactcA TGgctgactc ttcaacagac agtgctgacg aaggcccttc  
E6 cds ->  
241 tcctaagcgt agacatttag aagaagaaaa tacatctagc ttttagagc caccattacc  
301 agctacaatt cgtgaccctag ccaatctgtt agagatacca ttggatgatt gtttagtacc  
361 ttgttaacttt tgcggttaatt ttcttactca tttagaagg tgtgagttt atgagaaaaaa  
421 gcttagttt ctttggaaag atcattgtgt gttgcctgt tgcgtgtt gttgcgcagc  
481 aacagcgcaca tatgaatata atgaattttt tgaatctact gttgttaggtt gagatata  
541 agaaaataaca ggcaaatacta tttttgatata tgatgtcagg tgctacaatt gcatgaaatt



HPV21

3661 aataccgatt cagatccgga gggcaagtgt ccctcatcac taccgccacc accaccacca  
 3721 ccaccgcaac caactactcc accagagggt cagggcgagg gtcatactcc acctcctcc  
 3781 ccaccccaa acggccacga cggccacgag gagggggcat tggaggggac agtggggagg  
 3841 ggagacggtc atcctccacc tccccagcc cctccaaacg gtcacgagga aagttagt  
 3901 ctgttaggca acgtggcata tcctcgtacg acgtggaaa gtctttcaaa tcagtttagt  
 3961 caagaaatac aggtcgactt ggaagattac tggacgaagc tctcgatccc ccagTAAtct  
 <- E4 end  
 4021 tagtcagggg ggaacccaat acgctaaaat gcttcgcaa tagagccaag cttaaatac  
 4081 cagggttgc taaggcttc agtacggcct ggtcggtggt ggctggagat ggtactgagc  
 4141 gtctaggcag gtccagaatg ctcattagct tcttcctt tgagcaaaga aaagatttt  
 4201 ataagactgt taaatatccg aaaggtgtt accggctgta tggttccctt gatagcctaT  
 4261 AGcgcctT AAcatactaa ctatagctct gctactaaca tattaaact ttttgatTAT  
 <- E2 end  
 L2 orf start ->  
 4321 ATATttttttt ttatTTTTt tttttatgct ATGgcgcgtg ctaagcgagt caagcgagac  
 L2 cds ->  
 4381 tctgctacta atattacag aacctgcaaa caagcaggca catgtcccc tgatgttatt  
 4441 AATAAAgttg aaagcacaac tattgctgat aaaatattgc agtatggtag tgctgggtt  
 signal ->  
 4501 ttttcgggg ggctggcat aagcactgga aaaggtacag gcggtaccac aggttatgt  
 4561 ccttgggag aaggtcctgc agtccgtgtt ggcaatgctc ctacggcat tagACCTGCA  
 E2 binding ->  
 4621 TTGGTccctg acaccattgg cccgtctgat attattcctg tggacacccctt aaatccagt  
 4681 gagcccacaa cttcctctat tttccactc acagactcta caggcccaga tctgttacct  
 4741 ggagaagtgg aaactattgc agaaatacat cctggctcga ccaggcctcc acctgacact  
 4801 gcagtcacta cttagtacaaa tggctctagt gctgttttag aagtagcacc agagcctacc  
 4861 cttccctctc gtgttagagt aaccagaaca caatatcata atccatctt tcaagtaata  
 4921 actgaatcaa ctcctactac aggcgaaagt tcttagcag atcatatatt agtaacatca  
 4981 gggactgggg gacaaactat agggggcagt acacctgaac tcatagaact ccaggactt  
 5041 cttctagat attcatttg aatttgggg ccaacacctc ctagaagaac tagtacaccc  
 5101 attcaaagaa ttcaaaatata tataaggaga aggggtggcg ggctcacaaa taggcgttt  
 5161 gttcaacagg ttaatgtaga gaatcctttg tttgtatcca ggccttctag attagtgcag  
 5221 tttcaatttg ataaccctgc atttgaagaa gaagtgcacaa aatatttga gcaagatatt  
 5281 gatacttca atgaaccacc agatagagac ttttagata taaaacact tggtaggcct  
 5341 caatactcag aaACCCTGC AGGTtacgtg agagttgtc gtctggtaa acgaggaact  
 E2 binding ->  
 5401 attcgtactc gttcaggaac acaaattgg ttcgttgtcc atttttacag ggacccctag  
 5461 accattaaca cagaggaccc tattgaactt caattattgg gtgagcattc tggcgatgt  
 5521 acaattgtcc agggcccagt tggaaagcaca tttattgtata ttaacgttg tggaaaccc  
 5581 ctttctgaag atttttagtgc acattcagat gatttactt tagatgaggc aatgaagat  
 5641 ttttagtgggt cccaaatgtt ggttggaggc cgccgcctcc cttttctt tactgttcca  
 5701 cgttttggaa ctactagatc tggttcttat tacgtgcagg acaccaaggg ctattatgt  
 5761 gcctatccctg aagatcgaga cactagtaca gatataatct atccaaacacc agatttgc  
 5821 gttgtaatca tacacacatt tgatacaagc ggtgattttt acttacatcc gagtcttagc  
 5881 agaaaattta agagaagaag gaaatatttg TAAccctttc ttttgcagAT Ggcagtttgg  
 <- L2 end L1 cds ->  
 L1 orf start ->  
 5941 caagcagcta gtggtaaggt ttacccatca cccgtctacac cagttgccag ggtccaaagc  
 6001 acggatgaat atgtacaaag aacaaacatc tactatcatg catatagtga tcgcttatta  
 6061 actgttggtc atccatattt taatgtctat gacgtcaata gtcgtcaatgaaaatgt  
 6121 aaagtatctg ggaatcaaca cagggtattc agactcaat tgccagatcc taatagattt  
 6181 gcacttgcag atatgtctgt atacaatcca gacaaggaaa gattagttt ggcctgcaga  
 6241 ggtatagaaa taggaagagg gcaACCCTTG GGGGTggggaa gtgttaggtca ccctttattt  
 E2 binding ->  
 6301 aataaaatgtt gggacacaga aaatccatgt tcataaaaaa ctcaacccaa ttctactgt  
 6361 gatagacaaa atgtatcatt tgcattccaaa caactacaaa tggttataat aggctgtgc  
 6421 cttcgcttag gagaacattt ggtataagct atccatgtc caactgacaa tccacccctt  
 6481 ggatcgtgcc ctccgattgtc attaattat tcagcaatac aagatggcga tatggcagat  
 6541 ataqqatataq qcaatctaaa ttccaaqcc ttacaacaaa ataqgtctqa tggtagttt

6601 gacatagtttta atgaaacgtg taagtatcca gacttcttaa aaatgcaaaa tgatgtgtat  
 6661 ggagattcat gtttcttta tgcacgcaga gagcaatgtt atgccagaca cttctttgtt  
 6721 agaggggcga aaacaggaga tgacataccccc gcaggacaaa ttgatgaggg tagtatgaag  
 6781 aatgcattt acattccacc aatgaatgtt caagcacagt acaagattgg taactccatg  
 6841 tatttccaa ctgtcagtgg ctcattgggt tcttagtgacg ctcaattgtt taacaggcca  
 6901 ttttggctac agcgtgcaca agggcataat aatggcatat gttgggttaa tcaatttattt  
 6961 gttacagtag tagacaacac tcgtaacaca aacttttagt tttcagtaaa tcctgagaat  
 7021 gcagacgtgt ctaaaattgtt aaattataaa gccgagatc ttcaagaata tttaagacac  
 7081 gttaagaat atgaacttcc tttaatttttta caattatgtt aagttccccc aacagcagaa  
 7141 gtcttagctc aaattaatgc aatgaatgca aatatttttag aagaatggca gtttaggattt  
 7201 gttcctgccc cagacaatcc tattcatgtt acatatagtt acattgactc tgctgact  
 7261 agatgtcctg ataaaaaccc tccaaaagaa cgagaagatc cttataaaaa tatgaaattt  
 7321 tggatgttag atttaacaga acggttgtct cttagacttag atcaatatttcc ttggaaaga  
 7381 aaatttttat ttcaaggcagg tttgcagcag acgACCGTTA ACGGTacaaa gacactttct  
E2 binding ->  
 7441 tcaagggtat ctaccagagg aattaaacga aaacgcacaaa atTAGacatg ACCGTTTCG  
<- L1 end  
E2 binding ->  
 7501 GTacAATAAA gtcaactttt acacagtattt caaggaatgtt ttatttactc tgactaagca  
signal ->  
 7561 aaataccaaac cgccggcgcac acataaagggtt gagttgttag ccaaattgggg tgagttgtaa  
 7621 gccaaaagag gtcagagccaa agtctgttctt gagccagatc agataactacg cgccggcagag  
 7681 ttggatcaca tctcggtttt ctaacacgctt aaggactcaa ggaaatgtaa gtctgccaat  
 7741 cgattttggc tcgtgttttgc gcaaggatttt ggaccgtt  
 //

**HPV22**

LOCUS HPV22 7368 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 22, complete genome.  
ACCESSION U31780  
KEYWORDS .  
SOURCE Human papillomavirus type 22.  
REFERENCE 1 (bases 1 to 7368)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kremsdorf,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A.,  
Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G.  
TITLE Molecular cloning and characterization of the genomes of nine newly  
recognized human papillomavirus types associated with  
epidermodysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1013-1018 (1984)  
REFERENCE 3 (bases 1 to 7368)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV22 was originally isolated from macules on the chest of an  
Italian epidermodysplasia verruciformis (EV) patient [2]. The HPV22  
genome, like that of HPVs 9, 15, 17a/b, 23, 37, 38, is smaller than  
most PV genomes at approximately 7.4 kb. Phylogenetic  
reconstructions based on DNA sequences of established types  
indicate that HPV22 is most closely related to HPVs 23 and 38, and  
then to 15, 17, 37 and 9. Although Kremsdorf et al [2] found  
substantial cross-hybridization between HPV22 and HPV19, nucleotide  
sequence comparison fails to support a close relationship between  
these two types.  
BASE COUNT 2315 a 1352 c 1614 g 2087 t  
ORIGIN 149 bp upstream from beginning of E6 cds  
1 ccgccaaagc ttgccagg tttggcagaa catttgcgtt caaagactgc ACCGATAACG  
E2 binding ->  
61 GTaaaactt ttaattttta ACCGTAGGCG GTtattttttt attcgtagca acaattgtgg  
E2 binding ->  
121 tTAAcaacaa ttcctgcga gaatatacAT GcaACCGCTT GTGGTaattt atgcactgct  
E6 orf start -> E6 cds ->  
E2 binding ->  
181 tgcataattat ttaagttagga tggctgtcta ttctgttattc atggcttgc aaagaccact  
241 gacagtacag caacttagtg ataagttgac tgtacctgtt gtagatctt tgctaccttg  
301 tagattctgc agtaggtttt taacctattt ggaattgcgg caatttgatt ataagaattt  
361 gcaattaatt tggacagacg aggacttgtt gtttgcattt tgccggct gtgcctacgc  
421 ttcagcccaa tttgaatttc agcagtattt tcaagttact ttgtatggtc gtgaaattga  
481 gcaagaagaa caacgacctg taggccaat ttatatgaga tgtcaatatt gcttgaagtc  
541 tcttgatttg ctagaaaagt tagatatctg ctgttccaat caaccatttc acaaggtag  
601 agatcattgg aaggaaaggt gcaggcactg TAAagcaata gaATGAttgg gaaacaagct  
E7 orf start -> <- E6 end  
E7 cds ->  
661 actctgtgtg atatagttct tgaagagctt gtcctgccc ttgacactgca ttgccacgag  
721 gagctgcctg aacttccaga agagtttagaa gaatcagtgg tagaggagga gcctgagtag  
781 actccttaca agattgttgtt atattgtggg ggttgtgata caaagctgaa gctgttatata  
841 ctagcaactc tctctggaaat tcgcgacttt caaacatctc tacttggacc tgTAAactt  
El orf start ->  
901 ttgtgtccca cctgtcgaga agagattcgc aATGgacgac gaTAAaggta ctgacacaac  
El cds -> <- E7 end



## HPV22

4081 cgcgagcgcg aagaacaaag cgagcgtcag taactgacat ttataaaggc tgtaaggcct  
4141 ctgggacttg tccccctgat gttattAATA AAgtggaaca aaatacactt gctgataaaa  
signal ->  
4201 ttttaaagta tggcagtggtt ggtgtgttt ttgggtggtct tggtaagt acaggtaagg  
4261 gtaccgggtg tcctacaggc tatattccct taggtcaagg tcctggagt cgtgtggcgc  
4321 ccactccac agtggtcgc cccggggta tacctgaaat aattggacca actgaattaa  
4381 taccagttga ctcagtaaca ccaattgacc ctgcagcacc atccatagtg acattaacag  
4441 acagtagtgc aggtgctgac ctttacctg gtgaaggta aactattgca gaagttacatc  
4501 cggtcccaat agacaatgtg gaacttgaca cacccttagt ttctgggac cgtcagcc  
4561 ttttggaggt gactgatgt aatccccctt tttaggcac ggtagccac acacaatatc  
4621 ataattcctgc ttttgaattt atttcagat ctacaccatt aataggtaa tctacaccct  
4681 ctgaccatgt ttttgtttt gaaggctcg gagggttaca ggttagggat gctaattaaaa  
4741 gcattgaatt ggatacttt ccttcttagat atagtttga cattgaggag ccaaccctc  
4801 ctcgttaggt tagtacacca attgaaagaa tcagtcagga atttagaact ttaagaagag  
4861 ctttatacaa cagaagatta acagaacagg tccaagtaag agacccttg ttattcgtat  
4921 ccccggtccag gcttgtgaga tttcaatttga ataatccagt attcgatgag gaagttacac  
4981 aaatatttga aagagatgt agtcgactg aagaaccacc agacagggat ttttagata  
5041 ttgaaagact tggaaaggct atactaacag aaactgcaga agggcggtt cgtgtcagca  
5101 gtttagggca acgtgcacatcg ctgagcacac gcagcggcgc acgtgttagt gctagagtgc  
5161 atttcttac agatatttgc actattaaatg cagaagagcc cattgaatta gaattattag  
5221 gtgagcattc tggcgacagc tctgttagtac aagaaccatt tgaaagcaca atattggatg  
5281 tcaatatttga caacataacct gaaagtttgg atacaacat agcagaaaca tctgttagact  
5341 atgattctgc tgattttta ttagacaacg gtgtggagga cttagtagg tcacaatttgg  
5401 taataggcctt tcagataga tcacttccat ctattactgt tccacaattt gaatccccta  
5461 gagaaaccat tggtaacata caagacatag agggtaatac agttgtatat cctaaatatg  
5521 aagaaaggcc aactattata ttacctacac cctcggggcc tgctAAAtt caatcaccta  
L1 orf start ->  
5581 cacattcctc ctttgactat tatttacatc ctatgtcg aaggaaaaaa cgcaaacgc  
5641 aatatttaTA Atgttttca gATGaccctc tggctccaa cttcggtaa gatataatttgc  
<- L2 end  
L1 cds ->  
5701 cctcctacgc caccggtagc ccgagttacaa aacacggacg agtatgtgga gaggactgac  
5761 atctattacc atgctataag tgaccgttta ttaactgttag gacatccctt ctttgatgtt  
5821 agatcatcag atggagcaaa aatagaggc cctaaagtgt ctggaaatca gtttagggct  
5881 ttttagtagaa catttccaga tccttacaaa tttgtttgg gagatatgac aatccatgat  
5941 cccgaaaggat atagattatgt atgggcttggtaaagggttag aaataggaag aggacagccc  
6001 ttaggtgtatgtt accacagg tcatttcattt ttaataaaat tacatgatac tgaaaaccct  
6061 actgaacgc aagaaaggAAC atcagatgtt agaagaaatg tttctttgttgc tcttaacacag  
6121 gttcaaatgtt ttatcatgg atgtataccg ttttaggtt aatattggtaa taaagctcct  
6181 gttgtgaag atgcaggcag tcaggtagga ttatgtccctt cactagaatt aaaaatggt  
6241 gtatagagg atggagatgtt gtttgcataa ggattttggaa atataaataa taaaacacta  
6301 tcatttaataa gatctgtatgtt aagcttagac attgttaatgtt aatctgtaa atatcctgtat  
6361 tttcttacaa tggtaatgtt tggctatggc gactcatgtt tttttgtgc acgttagggag  
6421 caatgtttagt caccacacaa tttttgtacgt ggtggcttgc ttgggtatgc tataccagat  
6481 gatgcagttc aacaagatca taaatattac ttgcctgcag cttcacagac tgcttttagaa  
6541 aactccactt actttccaaAC CGTTAGTGGT ttttagtaa cctctgtgc ccaactattc  
E2 binding ->  
6601 aacaggcctt tttgggttga ggcgcgcgcg ggcataataa atggatatttt gtggaaacac  
6661 caaatgttttgc taacagtagc tgataataacc cgttaacacta attttcttat tagtgtggca  
6721 agtgacggca ccacagttaa ttatgtgtt aaaaaaaaaatca gagaatttttgc ggcgcattgt  
6781 gaagaataacc aattatcctt tattttgcag ctatgttagaa taccattaga agcagaggt  
6841 ttaactcaaa ttaatgcattt gatatgttgcg attttagaaaa attggcaact aggtttgt  
6901 cctacaccag acaattctgtt ccatgataact tataaggat tacaatctaa agtacaaaa  
6961 tggctatgtt ctgttacgtt caccacaaag gaagatccctt ttggtaata tactttttgg  
7021 aatgttagaca tggtaaaaa gttatcattt gatttagatc agtattccactt ggtcgtaaa  
7081 ttttttttttcaatctgggtt acaacgtgc aaggccagt ccagggtcag tggtaaaacgt  
7141 tctgctacgc ggaaaacgtc taaaactgtt aacacgtt aacttacctc tTAACCGTTT  
<- L1 end  
E2 binding ->

7201 TCGGTtgctt tAATAAAatc tattaactaa tctggtatgt gaagcatttt ttgaccacct  
signal ->  
7261 ttgtgactaa accgaacaag tcaacaccag caACCGCACC CGGTttttac attataaaatt  
E2 binding ->  
7321 cctcgaggta agataaccat cagtagatac catcggcacc tggagcaa

//

**HPV23**

LOCUS HPV23 7324 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 23, complete genome.  
ACCESSION U31781  
KEYWORDS .  
SOURCE Human papillomavirus type 23.  
REFERENCE 1 (bases 1 to 7324)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kremsdorff,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A.,  
Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G.  
TITLE Molecular cloning and characterization of the genomes of nine newly  
recognized human papillomavirus types associated with  
epidermodysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1013-1018 (1984)  
REFERENCE 3 (bases 1 to 7324)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV23 was originally isolated from macules on the forearms of a  
Polish epidermodysplasia verruciformis (EV) patient [2]. The HPV23  
genome, like that of HPVs 9, 15, 17a/b, 22, 37, 38, is smaller than  
most PV genomes at approximately 7.4 kb. Phylogenetic  
reconstructions based on DNA sequences of established types  
indicate that HPV23 is most closely related to HPVs 22 and 38, and  
then to 15, 17, 37 and 9. Strong hybridization was observed between  
HPVs 22 and 23.  
BASE COUNT 2331 a 1328 c 1592 g 2073 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 agcagataacc atcagcacct ggagcgaccg ccaagacttc gccaaacctgg cagaacattt  
61 gttggcaaga aaagagcACC GATAACGGTa agaactttta tttttgacc gtaggcgttc  
E2 binding ->  
121 atttactaac cttggcaaca atttgtggta acaacaatca taagccaata atacatgcaA  
E2 binding ->  
181 CCGCTTGTGG TAAtttattA TGcagactgt gcattattta agtaggatgt gctacaccaa  
E6 orf start ->  
E6 cds ->  
241 attattgatg gactcgacgc gACCACTGAC GGTacagcaa cttagtgata agttgacagt  
E2 binding ->  
301 accagtggta gatctctgc taccttgcag attttggat aggttctta cctattttaga  
361 gttgcgagaa ttgttattata aacatttgca gttaatctgg acagaagaag attttggatt  
421 tgcattgtgc agtggctgt cttatgttc tgctcaattt gaaattcaac aattttatca  
481 gctaactgtg tatggctgtg aaattgagca ggaggagcaa cgacctata gccaaatttg  
541 tatttaggtgt cagtattgtt tgaagtctct cgatttgata gaaaagctag atatctgttag  
601 tttaatcaa ccatttccaa aggttagaaa tcatttggaaag ggaagggtca ggcatttgTAA  
E7 orf start ->  
661 ggaaatagaA TGAttggaa acaagctact ctgcgtgata tagttcttga agagcttgc  
E7 cds -> <- E6 end  
721 cagcccattt acctgcattt ccacgaggag ctcactgaag aggttagaaga agcagtcgta  
781 gaggaggagc ctgaatacac tccttacaag atcatcgtag tttgtggagg ctgtgagaca  
841 cagttaaaacg tttacgtgtc agccacagat tttggattt gctcgttcca agcatcttt  
901 ctagaaaaacg TGAagctgggt gtgtcctgcc tgtcgagaag acattcgcaA TGgacgacga  
E1 orf start -> E1 cds ->  
961 TAAaggtaact gatactgcta aagaaggctg tagtacttgg tgcttattag aggctgcttgc  
<- E7 end

1021 ttctgatgat agtgacccat atgatagttt ggagaaattta tttgaagaga atgcagagtc  
 1081 agatgtgtct gatttaataa atgatgatga taatgtctgt caggaaaatt cccgcgaatt  
 1141 gctatgtcaa caggagagtg aggaatgcga gcagcaaata caatacctaa aacgaaagta  
 1201 taatatcagt ccagaggctg ttcagcagct tagtccacgt ctacagtctt tgaatttgc  
 1261 gcctggcat aaatctaaaa ggagattgtt tggagcaaa gacagccgac tggagttatc  
 1321 tctaaatgaa gttgaagatt ttactcaaga gttggaggtt ccggcgagcg ctccaggccc  
 1381 ggcagcccag ggtggagtag ggctggaca tattgaaagt ttgtaagat gtaaaaatgc  
 1441 taaagcagtg ttgctacata aatttaagga aggttttggg attagttata atgagcttac  
 1501 cagacagttt aaaagcaata agacctgctg taaacattgg gtattggcca tatatggtc  
 1561 aaaagaagag ctcatagatg cgtctaagca attgttacaa cagcactgtt ctatatttg  
 1621 gttgcagaca tacacacca tgcacttta ttatgttgc tttaatgttgc caaaaatgt  
 1681 agaaacagtt gtaaaattat tgatttctat gctgcaaata catgaaaatc atatattatc  
 1741 agaacctccg aaaaacagaa gtgtacctgt agcttattt tggtaaaag gcagtatgaa  
 1801 ccttaatgta tatgcatttg gtgagtatcc tgagtggatt gtgacacaaa ccatgataca  
 1861 acatcaaact gctgacagta tacaatttga ttgtctcgat atgattcaat gggcctacga  
 1921 taatgatcat cttgacgaat gtgtatttgc ttataactat gcaaatttgg ctgacacaga  
 1981 cagcaatgca agagctttt tagctcaaaa tagccaagca aaacatgtaa gagattgtgc  
 2041 acagatggtt aagcattata aaagaggtga aatgcgagaa atgactattt ctgcattgggt  
 2101 acatcattgc atatctagaa ttgaaggtga tggacaatgg caagatattt taaaattttt  
 2161 ggcgtatcag ggattaaact tcattgtatt tttagataaa tttagaacgt tttcacagaa  
 2221 tttccaaaa aaaaatttgtt tggtaatata tggccctcca gacacaggca aatcaatgtt  
 2281 tactatgtct ttaatgaaag cactaagagg tcaagtaata tcgttgcattt attctaaaag  
 2341 ccaattttgg ctgcaaccat tagctgatgc aaagatgcgc ttattagat atgcaacaga  
 2401 agtttggttt caatatatttgc atatgttct tcgaaatggg ttggatggta atgtatgtc  
 2461 gttggatatg aaacatagag caccatgtca aatgaaattt ccaccattaa ttattacatc  
 2521 taatatttagc cttaaagaaag aaaagaagtt tccttacttg catagtagaa tatatgaatt  
 2581 tgaatttcca aacagatttgc catttgcattt agatgataaa cttttttta aacttactgaa  
 2641 ccaaagctgg gcgtctttt taaaaggct ttggatacaa tTAGgactca gtgaccaaga  
 E2 orf start ->  
 2701 ggacgagggaa gaggATGgaa gcactcagcg aacgccccat tgcactacaa gacaagttaa  
 E2 cds ->  
 2761 tggacctgta TGAatcggt ttagaggatc ttgaaactca aatacagcat ttgaaactct  
 <- E1 end  
 2821 taagacaaga acaaatttta ttgtattatg ctgcggaaacgg tggattatg cggttgggggt  
 2881 accagccggc accctcctcg gcaacatcg aatattaaagc aaaagatgct atagcaatttgc  
 2941 gaattttgct ggaaagttt caaaaatcca aatatgcaga tgagccatgg acattagtt  
 3001 agactagctt ggagacaattt agaagtcac cagTAGattt cttaaaaaag ggacctaaaaa  
 E4 orf start ->  
 NH<sub>2</sub> terminus unknown  
 3061 cagtggaggt gtatTTTgtt ggagatccgg aaaaatgtt gcccataataca gtatggtctt  
 3121 atatTTTacta tcaaactgtat gaggacactt gggaaaagggt tgaaggacat gtggattata  
 3181 caggagctt tttttagat ggcacactt aaaaacttta cattaaattt gaagcagatg  
 3241 caaagcgctt tggacttaca ggaatgtggg aagtacatgt taataaagat actgtcttta  
 3301 cccctgttac tagttctacg cccgcggatgg gagacgcctc caacaacgcgtt gttcccgaaag  
 3361 catctaccac ctccttgc tccccacaac ggtcaccatc caccaaccgc cgatacgcc  
 3421 gaaaagcatc tagccctaca gccaccacca ggaggcaaaa aagacaagga aaagaaaaccc  
 3481 tcaccaggcg aagaaaaacc agatcaaggt cccggagcag agagcaacgg gggggggagg  
 3541 aaacccaaag atccctccccc agaggagcct caaaatcccc ccggccgggaa gggagaagtg  
 3601 gagggggggcc cctcaccaccc tccagatcaa gatccagatc accagagtct gttacagggg  
 3661 gtggcgttgc accttagtggaa gtggagcgt cacttcgttgc agtttagtgc cacagtagtgc  
 3721 gaagacttgc gcaactattt gatgcagctt aagacccccc agTAAtatttgc ctgcgcggcg  
 <- E4 end  
 3781 gtgcaaatac attaaaatgc tatcgctata gtttttagaaaa aaagcatgct ggtttttttt  
 3841 attatgttag cacaacgtgg tcatggattt ggggtcattt tactgataga gttagggcgt  
 3901 caaggatgtt aatagcattt cattctaatc atgaaaggaa aaaatgtattt caagaaatgt  
 3961 agttacctt aggtagat tggccatgtt gacaatttgc tgattttAA cctgtttttt  
 <- E2 end  
 4021 attTAACaca ctaacattgc ctattgtat ttttttacta acttatatttgc tttatattgt  
 L2 orf start ->

**HPV23**

4081 actaacattA TGgtacgggc gcaaagaact aagcgagcgt ctgttactga tatatacaaa  
L2 cds ->  
4141 ggctgtaaag cctctggac ttgtccccct gatgtactaA ATAAAGtggA acaaaaataca  
signal ->  
4201 ctgctgata aaatacttaa atatggcagt gttgggtgtt tttttgggtt acttggatt  
4261 ggtacaggta agggtaccgg tggtgccacg gggtaacgtcc cattgcgacc tggagtcga  
4321 gtggcggtta ctccctacagt ggtccggccct gcagtcatac ctgaaataat tgaccact  
4381 gaattaatac cagttgactc aatagcacca attgaccccg aagcaccatc aatagtctca  
4441 ttaacagaca gtggcgacgc tgctgaccc ttccccagtg aagcagaaac tattgcagag  
4501 gtacatccta cacctgtaga cataggaatt gatacaccta ttgttagctgg aggccgtgac  
4561 gccatTTtag aggtggtaga tactaatcct ccaacaagg tcaagttaac aagaacacaa  
4621 tatgataatc catctttca aataattca gaatccacac ctatcacagg tgaggcatcc  
4681 ctgctgatc atgttattgt gtttgaaggt tctggaggc agcagctagg agccgttaact  
4741 gaagagattt aatttagatac atatccttcc agatattcct ttgaaattga ggaagctaca  
4801 ccaccacgca gaactagttac tcccattgaa agaataagtcc aggaattcag gAACCTACGT  
4861 agagcactgt ataacaggcg cttaacagaa cagggtcaag taaaaaaccc ttatTTTta  
4921 actactccat ctaaaacttgt aagatttcaa ttgtataatc ctgttttga tgaagaggtc  
4981 acacaaatat ttgaaagaga tggtgctgaa gtggaggaac ctccagatag ggacttttt  
5041 gatatacgaca gatttaggaag accattatta acagaatcca ctgaaaggccg tattagatta  
5101 agtaggttag gtcaaaggcc ttccattcaaa acacgcgtg gaacacgtgt tggttcacgt  
5161 gtacacttct atacagattt aagcactatt aatacagaag aacctataga attagaatta  
5221 ttaggcgagc attctggaga tgcattcattt attgaggaaac ctctgaaag cactgtata  
5281 gatatacgact tagatgtatgt tgaggctatt caggatacta tagatactgc agatgattat  
5341 aactctgcag atctttattt ggacaatgca attgaagaat ttaataattc tcaattatgt  
5401 ttggcactt ctgatagatc ttcgtctgca tattctatac cacgggttga atccccataga  
5461 gaaacaattt tatagttca agatatagaa ggtatcagg taatttatcc tggcccaca  
5521 gaaaggccaa ctataatattt tcccttacctt agtgccttgc ctgttagtcat acacacattt  
5581 gacaagtctt ttgatttattt cttacatccc agctTAAGaa agaaaaggcg caaacgcaaa  
L1 orf start ->  
5641 tatttaTAAAt gttttcagA TGaccctctg gcttccagct tctggtaaga tatatttacc  
<- L2 end  
L1 cds ->  
5701 tcctacgcca cctgttagcc gagtgcagag tacggatgaa tatgtggaaa gaactgacat  
5761 ctattaccat gcaacttagt atcgattactt aactgttaggc cacccatatt ttgatgttag  
5821 atcaccggat ggttagaaaa tagatgtacc aaaggttca gggaaatcaat tcagggcctt  
5881 tagagttaca ttccagacc ctaataagtt tgcattagca gacatgacta tctatgatcc  
5941 tgataaatac aggttgggtt gggcctgcgc aggacttggaa atcggccgcg gccaACCTTT  
E2 binding ->  
6001 AGGGGTcggc agtacaggac acccgctatt taataagctc cgtgatgcag aaaattcttag  
6061 tgaacgtcag gaaggtaactg tagatgacag aagaaatatac tcattgtatc ctaagcaagt  
6121 acagatgtt ataattgggtt gcacaccgtt cttaggtgaa tattggata cagtcctgt  
6181 ctgtaaagat gcaggtagcc aactagggtt gtgtcctctt tttagattaa aaaacagtgt  
6241 tatagaagat ggggacatgt tcgacattgg ctttggtaat atcaataataaa acatttac  
6301 cttaataga tcagatgtt gtttagatct tgtaaatgag gtttgc当地 atccagactt  
6361 ttgtactatg tcaaattatgt tatatggaga tgcctgtttt ttttggccc gaagagagca  
6421 atgctatgcc aggcactatt ttgttcgagg cgggttagta ggagatgcaa tacctgtatgg  
6481 tgcagttcaa caggatcaca aatatttattt acctgcagac caacaaaaca cttagaaaa  
6541 ctcactttat ttccctactg tcagtgatc tttggtaact tctgttctc aacttttt  
6601 tagaccattt tggtaaaac gtgcataagg ccataacaat ggtattttat ggaacaacca  
6661 gatgtttgtg actgttagcag ataatacagc taatacaaaac tttagatca gtgttaccaa  
6721 tgacagcgtt ttagaaaatgt atgatgccat taaaattttaga gagtttacaa gacatgttga  
6781 agaataccaa ctttcttta tactacagtt gtgcaggata cttttaagg ccgaggtctt  
6841 aacacaaattt aatgccatga attcagatattt tttagagaat tggcagtttag gtttggcc  
6901 tacaccagat aatgcgttcc atgacacata cagatatttgc gttcaaagg ccacaaaatg  
6961 tccagatgca gtacctgaca cgaaaaaaga ggatcctttt ggaaagtattt cattttggaa  
7021 ttgtatgtt acagaaaaat tgcctctaga cctagatcaa tatcccttag gccgtaaatgg  
7081 tctgtttcaa attggagtgca agcgtgtacg gtccggatcc aaacggcctg caactcgaaaa

11

**HPV24**

LOCUS HPV24 7452 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 24, complete genome.  
ACCESSION U31782  
KEYWORDS .  
SOURCE Human papillomavirus type 24.  
REFERENCE 1 (bases 1 to 7452)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kremsdorff,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A.,  
Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G.  
TITLE Molecular cloning and characterization of the genomes of nine newly  
recognized human papillomavirus types associated with  
epidermodysplasia verruciformis  
JOURNAL Journal of Virology 52 (3), 1013-1018 (1984)  
REFERENCE 3 (bases 1 to 7452)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV24 was originally isolated from macules on the breast of a Dutch  
epidermodysplasia verruciformis (EV) patient [2]. It hybridizes only  
weakly with other other EV-related HPVs [2]; phylogenetic analysis  
of DNA sequences indicates that HPV24 is clearly most closely  
related to EV-related types, but it is not closely related to any  
particular subgroup.  
BASE COUNT 2385 a 1352 c 1629 g 2086 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 ggcggcaagtt tcttggcact cgccacagcAC CGTTAACGGT aagtgttttg tatactgtac  
E2 binding ->  
61 cgggcgcgat accaaatatg ccacacctgc aattgttgtt agcaactact ttcattaccct  
121 aacaaggatt ttcatgcacc gttccgtat cactgtgaat gtatttattt atTAGacaTA  
E6 orf start ->  
signal ->  
181 TAAAAaggaa gacatcttgA TGgctcaacc aggttaaacct cagtcagtgt tagaacttag  
E6 cds ->  
241 tagattatta aatataccat tagacgattt tggtgtacca tgtaactttt gcaaaaagatt  
301 tctaagttat acagagttaa ctgactttga caccaaatgc ttaagttga ttggaaaga  
361 cgattttgtg tttgcattt gtatgttgc ttgtgttgc acagcagcat ttgaatttga  
421 aaatttatttt gtatgttgc ttgtgttgc ggaaatagaaa caaaaagaaaa atacaccctct  
481 ttccggacatt attgttaagggt gtcaccattt cttaaaattt cttaatcaaa ttgaaaagct  
541 tgatatctgt ggaagatctg aatttatttca taaatgtgagg aggggctgga aaggactctg  
601 taggcagtgtT AAAGcagataT AATGatttggaa aaaggaggta ctttacaaga catttgtctta  
E7 orf start -> <- E6 end  
E7 cds ->  
661 gagttgactg agcccacagac tggttggattt cactgtgaag aggagttgcc agagcaggat  
721 acggagggtgg agcctgaaag aagagcttac aaaataatac ttgttgcgg cggcggttgc  
781 ggaacccggc ttgcatttatt tttgttgc acacatgttgc gaatacgtgg ctttgcagac  
841 ttactgcTAG aagagggtgtt cttttgtgtt cccgactgcc gtaacagcga tctgcagcAT  
E1 orf start -> E1 cds ->  
901 GgcggacaaT AAAGgttagtg aaacagacgg gttgcatttgc ttgtgcttat tagaagctga  
<- E7 end  
961 ctgttagtgat attgaaaatg atttggacac attgttgcgg caaaaattcag attctgtatgt  
1021 atcagatctt ataagtaatg atggggactt ggaacaggaa aactcccgg aactgtttca  
1081 acaggaggag ttagaggaga gcaatgtttt gttgcaaagt ctaaaaacgaa agtatattag  
1141 tcctaaagct gtattacagc tgagtccaca acttgaatcc atttcgtgt catcagacca

1201 taaaactaag aggaaattgt ttgctgagca ggacagtgg a tagaattga cccttacaaa  
 1261 taaaactgaa gatgttacta cattggcga gcaggaggaa gaggttaccag cttagagac  
 1321 atcttccacc agtaacttaa ggaaggaga taatgcacat tataaagaac ttatgcgtg  
 1381 cagtaactta aaagctacct tactatcaaa attaaaaat gctttggtg taagcttgc  
 1441 tgaactgact cgccagttca gaagtaataa gacttgggt aatgattggg tgtagcaat  
 1501 atatggtgta aattatgatt tatttggaaag ttctaagcaa ttactacaac agcattgtga  
 1561 ttatatttgg gttacagaaa tgtctgcaat gtttttatat ctgttggtt tcaaggctgg  
 1621 caaaaataga caaactgtta taagttatt agtgtctatg ttatatgtgg cagaggagca  
 1681 aattttatca gaacctcaa aattgcgaag tacagtgtca gctttatgg ggtataaagg  
 1741 tagctcaa at gctgttaccc ttacacatgg gtcttatcc aatggatta tagaacaac  
 1801 actgatagga catcaaacag gagaagctgc aacgtttgac atgtccacaa tgtagtataatg  
 1861 ggctttgtat aatgatctca cagaggaagc tgacatagct ttcaatatg caaagctggc  
 1921 acctgatgat gtaaatgcaa ctgttgggtt ggctcacaat aatcaggcgc gttttgtaaag  
 1981 agaatgtgct aatatggta gatattataa aaaaggttag atgcgagaaa tgtagtgc  
 2041 ggcattggatc cactttaaat tagacaatg agaaggggaa gggcagtggt caactattgt  
 2101 aaaaatttatt aggtatcagg gtataaattt tattatgg ttaagtgc ttaaaagattt  
 2161 ttacatggt aaacctaaaa agaattgtt attatataat ggcctccaa atactggaaa  
 2221 atcagcattt actatgtcat taattaaatg gttgcattggc agagtaatat catttggaaa  
 2281 ttctaaaatg cactttggt tgcaaccaat gtctgaagcc aaaatagctt tacttgc  
 2341 tgctactgat ccatgttgg tatataatgg tacatattt agaaatggc ttgatggaca  
 2401 cttagttca ttagattgtt agcataaaagc acctatacaa atacgcttc ctccattact  
 2461 tataacatct aatattaatg caatggcaga acctaactat agatatttac acagtaggtt  
 2521 agtagcggtt gaatttccta atcccttcc tatgaaaatg gacgataccc ctgaatttga  
 2581 acttactgac caaagctgg aatcttttt taaaaggctt tggagacaat TAGacctcag  
 E2 orf start ->  
 2641 tgaccaagaa gacgagggag aggATGgaga acctgaaaaa gcgttgcgt gtgttgc  
 E2 cds ->  
 2701 atctactaat gaacatttaT GAacaaggca gtgatacact agaattcacaa attgaacatt  
 <- E1 end  
 2761 ggcaggccctt ggcgaagagag gcaagtgttac tttattatgc tagacaaaat ggggtgctgc  
 2821 ggctgggtta cttaccagtt ccaccactag ctacctcaga agccaaagct aacaggcta  
 2881 ttagtatggt gttcagctg caatcttac aacaatctcc ttatggcaca gaaaagtgg  
 2941 cactggtggc cacaagcata gaaaccttta aaaatactcc agagaaccat tttaaaaaag  
 3001 gacctataaa tggaggtt atatatgtt gtatccggc caatgccaat ttgtataacta  
 3061 tggaaaata tggatattat atggatgata atgaccatgt gaaaaaaaaact gaaagtggc  
 3121 ccaatcatac aggcatatata tattaaTAG gggagttaa acattattat gtgctgttt  
 E4 orf start ->  
 NH<sub>2</sub> terminus unknown  
 3181 ctgatgatgc caatagatac agtaaatctg gccaatggg ggtcaggatt aataaggaaa  
 3241 ctgtttgc ccctgtcacc agctccacac caccggactc cccaggaggg tcccgagaac  
 3301 taccggatc caccgtaac tccaaggcc caagcccaac ccaacagcca caacaaggct  
 3361 gtagtgacga aacaaccaag cggaaagaggt acggggcgaag ggagtaagc cccactgact  
 3421 ccagatgcag acgacgatcc tcgtccccggc aaaagaagcga agggcgcacga gcacggtccc  
 3481 gcacccggc gcgctgcac tccactcaa ctgcgtctag atccaccta aggaggtcca  
 3541 gatcaacctc caggggcaac aggagggtt ggggagacac ccccgagggg caacggagg  
 3601 tctcaacctc ctccaggggg aggggaaagg gcaactgaaat gtcatccctcc tcctccccc  
 3661 ccaccccccag aaccaaagcc tcacaacggg gatgcgcac acggctgtt agggacagt  
 3721 gcatctctcc tggggacgtt ggaagaaaac ttccagacagt tagtggaga aattcaggaa  
 3781 gacttggacg attattggag gaggctctcg atccccagT AAtttactt cgtgggggt  
 <- E4 end  
 3841 ctaacacatt aaaatgtttt cgcaacaggg caaagcttag atatagagga cattataaag  
 3901 cattttagcac atcttggtca tgggttagctg cagatggcac agagcgtcta ggcagggtcca  
 3961 gattgctcgat cagtttacc agtttaacg agcgaagtgg gtttctcgac ctatgtt  
 4021 ttccctaaggg tggatattgg tcactggaa gtttgcataa actgTAAGta ctaacatagc  
 <- E2 end  
 4081 ttttgcacT AAacacacata taacctattt ttactttttt tatgcttgc aATGgtgcgt  
 L2 orf start -> L2 cds ->  
 4141 gctaaaagaa caaaacgaga ttctgctact aatatttaca gaacatgcaa gcaggcgggc

## HPV24

4201 acatgtccac ctgatgttat tAATAAAgtg gaacagtcaa ccattgctga taatatactt  
signal ->  
4261 aaatatggaa gtgctgggt ctttttggt ggcctgggt ttagtacagg ccgagggact  
4321 ggaggcacca caggatatgt gccattgggt gaaggtaactg gagttcgtgt gggcagtaca  
4381 cccacagtcg ttccggctgc ccttgtgcct gaagtaata tagtcctct tactgaatca  
4441 gttgatacaa tagccccgt tgacccagca tcgtcatcta tagttcctct tactgaatca  
4501 tcaggtgttag accttttacc tggtaaaata gaaacaata tagaagtaca tcctataacct  
4561 gatgtgccca catttgatac tccagtagt acaacaagca aaggctctag tgccatttta  
4621 gaagtagctc ctgagccatc tccaccgaca cgtttcgta tcagcagaac acaataccat  
4681 aatccagcat ttcatattat tacagaatct acaccaagt aaggtgagag ttcattgtca  
4741 gacgaaataa ttgtcgctc tggtgccgt ggacaatcg taggcgttc tggaaatata  
4801 gaactgcagg atttatcaaa tagatattct tttgaaatag aaacaccaac accaccaagg  
4861 cgttagcaga cccattaca aagagctaca caagcattta gacaagatc acttacaaat  
4921 agagactgt tacaacaatg gcctgttga gaccctttgt ttttaactca accatctaaa  
4981 ttggtagat ttgcatttga gaatccagct tttgaagagg aagtaacaca ggtatttgaa  
5041 caagacctt caggtttgt agacccctt aacagagatt ttttagat tgcagaactg  
5101 ggaaggccta gatttctga aacacgcgag gttatgtt ggttaagcag attgggtcgt  
5161 agagcaacta tttagaacaag ggcaggaaca caaataggag cacaagtaca ttttataaaa  
5221 gatctaagtt ctattaatac tgaagctcct attgagttgg atcttttagg gcagcattct  
5281 gggatgcaa ctatagttca tggactgt aaaaacat ttatagatac taatataag  
5341 gaaaatcctt tagctgaaca aatggagttg gaaattgata cttatcctga agtcattca  
5401 tttgatgctt tggtagatga agcaacagac gatttttagt gttcacagtt agttataggc  
5461 aatagaagat ccactacatc atatactgtt cctagattt aatccccaaag aaattcttct  
5521 tattatgtac aggatttgcg gggatattat gtagcctatc ctgaatctcg cgataaaaata  
5581 gaacttattt atccctcacc cacattacct gcagttgtca tacatacaga agatagtagt  
5641 gggactttt atttacatcc tagtttattt caaaggcgcg gacgcaaacg aaaatatttgc  
5701 TGAaaaaatc agATGtcggt gtgggttgcgc gccagttgtt aggtatattt gccaccatca  
-< L2 end  
L1 orf start -> L1 cds ->  
5761 acacctgttg cgaaagttca aagcacggat gaatacatac agagaacaaa catttctat  
5821 catgcttata gtgaccgcct attaactgtt ggacacccat attcaatgt ttacaacaat  
5881 gatggcacag tattagaggtt ccctaagggtt tcaggaaatc aacacagagt ttttaggctt  
5941 aaattaccag accctaatacg atttgttta gcagatgtt ccgtatataa tccagagaag  
6001 gaaagattgg tatgggttg cagaggatg gaaataggta gaggacaacc attaggttt  
6061 gggacaagtg gacatccattt atttaacaaa gtgaatgaca cagaaaaccc ttttatcatat  
6121 aggacacaag catcgtccac agatgataga caaaaatccat catttgcatt taaacaaaatt  
6181 caaatgttta ttataggtt tgccaccctgc ataggagaac attggaaagt agctgagagg  
6241 tggctgggtt ataataatgt tgctggtaga tggccaccata ttaagttgtt aaattcagta  
6301 attcaagatg gtgatatggc agatattggt tatggaaatt taaattttt aacactacaa  
6361 caaagtagat cagacgttcaag tttggatattt gtaaatgaaa cctgttataa tccagacttt  
6421 taaaaaatgc aaaatgttgc ttatggatgt tttttttt tctttgtcg ccgtgagcaa  
6481 ttttatgcaaa gacattttt tgcgtggg ggttaaacccag gggatgacat acctgggttag  
6541 caaattgtatg cagggaccta caaaaatgc ttatccattt cagcagccac aggtcagac  
6601 caaaaataa ttggcaactc aatgttattt ccaacagtc gttgttgcatt ggtatctat  
6661 gatgtcaat tatttaatag accattttgg ttacagcgtg cacaaggta taataatgg  
6721 atttggggg ctaatcaattt gttcattacg gtagtagata acaccaggaa cccaatttt  
6781 agtataatgt tataactgtt aatggcaaa gtaacagata ttaacagata tgatgctaat  
6841 aaatttaggg aatatacgatg acatgttagaa ggtatgaaa tttcactt actgcagct  
6901 tggaaaaatcc cttttaaaagc agatgtgtt gcaacatca atgctatgaa tccatctcta  
6961 ttggaaagagt ggcagttagg atttgcctt gcaccagaca atccttca aagtacctac  
7021 agatataatgt aaagtttgcg aacacccgtt ccagataaaag tagctccaaa agaaagagaa  
7081 gatcctttagt ccccttatac gttttggat gtagattttt ctgaacgctt atctttggaa  
7141 ctggatcaat attcctttagg acgaaagttc ctgtttcaag cgggtttgtt aaaaaaaaaaca  
7201 tctaaaaaaa catctaatgtt atccaagggg accaaacgaa aacgcacgTA AAATAAAAgc  
-< L1 end  
signal ->  
7261 tggggACCGT TTTCGGTaca atatatgtgtt attccaagaa tgcttggat tcatgtgcgt  
E2 binding ->

7321 gactaatttg aactttggct tgaatgtcaA CCGCACCCGG Tacaagttaga taaaatcttg  
E2 binding ->  
7381 ctaccacagc agacacaaag gaatcactgt cggtctcaac acgctcgat ttggcgcatt  
7441 caaccgttt tg

//

**HPV36**

LOCUS HPV36 7722 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 36, complete genome.  
ACCESSION U31785  
KEYWORDS .  
SOURCE Human papillomavirus type 36.  
REFERENCE 1 (bases 1 to 7722)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Kawashima,M., Favre,M., Jablonska,S., Obalek,S. and Orth,G.  
TITLE Characterization of a new type of human papillomavirus (HPV)  
related to HPV5 from a case of actinic keratosis  
JOURNAL Virology 154 (2), 389-394 (1986)  
MEDLINE 87020745  
REFERENCE 3 (bases 1 to 7722)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT DNA of HPV36 was extracted from biopsied lesions of 2 patients with  
actinic keratosis (AK) and molecularly cloned; 22 other patients  
with AK were HPV-negative by blot hybridization to a range of  
HPV-types. The HPV36-positive patients were an 89 year old man  
(patient A) and a 61 year old man (patient B) with one lesion on  
the head and multiple lesions on the backs of hands and fingers  
respectively. Patient B also had a squamous carcinoma on the  
forehead. In patient B, HPV DNA was detected in only two of seven  
lesions of the hand and not from the sqamous carcinoma. HPV36 DNA  
was not detected in many other skin lesions in the general  
population (22 samples of Bowen's disease, 12 squamous cell  
carcinomas, 21 basal cell carcinomas, 8 keratoacanthomas). In  
contrast, HPV36 was found in 7 of 18 epidermodysplasia  
verruciformis (EV) patients known to be positive for HPV5 and at  
least one additional EV-associated type. The low rate of detection  
of HPV DNA in AK lesions in the general population allows for the  
possibility that HPV36 was not a causative factor in those AK  
lesions where it was detected. Nevertheless, HPV36 was the first  
example of an EV-associated type to be detected in an  
immunocompetent non-EV patient. Blot hybridization unde stringent  
conditions revealed significant cross-hybridization only with  
certain EV-associated types (HPV 5,8,12,14,19-23,25); no  
cross-hybridization was detected with the other EV-specific HPVs  
(9,15,17,24), nor various non-EV cutaneous types (1-4, 7, 10,  
26-29, 34), nor variousmucocutaneous and mucousal types (6, 11, 13,  
16, 18, 30-33,35). Phylogenetic analysis of DNA sequence indicates  
that HPV36 is most closely related to HPVs 5, 47, 8 and 12.  
BASE COUNT 2337 a 1497 c 1773 g 2115 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 gtaagttatt taatttatgt ACCAGGTGCG GTactggaat ttcacaataa taatttgttgc  
E2 binding ->  
61 tgccaaactac cattgctata ttcaagtttt tgcctgtatc gttttcgat catgtgaata  
121 atatactgtat tagTATAAAat aaataaataa atatatataat atatgcttca aagggttgggt  
signal ->  
dinucleotide "TA" repeat region ->  
181 tttttaaTAA ttaaggcaaA TGgcagagca agcctccgaa cagcagaata ttacagaaaa  
E6 orf start -> E6 cds ->

241 agaaaaagaa cagctgcctt taactattaa gggcctgtca gaatcattag gcattccgtt  
 301 ttagactgt ctaatacctt gtaacttttggcaaaattt ttagattatt tagaagcttg  
 361 tgagtttaggat gttaaaaaggc tttagttaat ttggaaaggat tactgtgtat ttgcctgtcg  
 421 tcgtgttgttgc tttgtgtgc cagccacata tgagttaat cagttttatc agcagacagt  
 481 attaggaaga gatattgaat tggctgcagg tcgctccata tttgaaattt acatttagtg  
 541 tcagacgtgc tttagcttc ttgacataat tgagaagtTA Gattgtgtg gaagaggact  
 E7 orf start ->  
 601 tccctttcat agagtcgaaa acgcctggaa gggaaatctgt aggcagtgtt aacatttttta  
 661 taATGattgg TAAagaggtc accgtgcaag atattgttct ggagctcagt gaggtgcagc  
 E7 cds -> <- E6 end  
 721 ctgaagtact accagttgac ctgttttggta aagaggaattt accaaacacg gatacggagg  
 781 aggagcttgc caccggaaaga atcgttttca aagtcatgtc accgtgtgt tgcatggccact  
 841 gtgaggtcaa gctccgcgtt tttgtccaag ctacagaattt tggcatcaga gcattcaac  
 901 agttgcTGAc cgggtgacatc cagttctgt gtcccgagtg tcgtggaaac tgcgaacATG  
 E1 orf start -> E1 cds ->  
 961 gccgatccTA Aaggtagtac atctaaagaa gggtttgggtt attgggttat tttgaaagct  
 <- E7 end  
 1021 gactgttagt atatagaaaa tgatatggaa caattatttggaa aagagatac agattctgtat  
 1081 atttcggact taatagatga ttgtgacactt gaaacaggaa attctttggaa actatttcac  
 1141 caacaggagt gtaaggcagag cgaggagcaaa ttacaaaaac taaaacgaaa gtgtcttagt  
 1201 cccaaaagctg tcgcacagct tagtccgcga cttcagtcaa ttcatgtc acctcagcag  
 1261 aagtctaaagc gaaggcttgc tgcagagcag gacagcggag tcgagctgac cttaaacaat  
 1321 gaagctgaag atgttactac tgaggtggag gtaccggcta tagactctcg gccggatgac  
 1381 gaggggaggat cagggggatgt agatatacat tatcttcac tggcgttc cagcaacaaa  
 1441 aaagccacat taatggcaaa atttaaagca gcgttgggg taggcttaa tgaattgaca  
 1501 cgtcaattca aaagtccaaa aacctgctgt aatcattggg ttgtctctgt ttatgcagtc  
 1561 catgtatgtc tatttggaaat ttcaaaagcag ttgttgcac acgattgtga ctattttatgg  
 1621 gttcgtggaa tagatgcaat gtcattatatttgtt ttaaggcggg aaaaaatcg  
 1681 gggacagtgc ataagttgtat gacttcaatg ttaaatgtgc atgaacacgca gattttgtct  
 1741 gagcctccaa agttaaagaaa tactgctgtc gcattttttt ggtacaaaagg ctgtatggaa  
 1801 tcgggggtgt tcagttatgg gccatatcctt gattggattt cacaacacat tatatttagt  
 1861 cacaataatg ctgaagcaag cacctttgtat tttcacaga tggtacaatg ggcctttgtat  
 1921 aatcagttatg ttgtatgtt gatatttgc tatcgatatg caaggcttgc accagaagat  
 1981 gccaatgtcg ttgcattgtc tgcacataat agtcaagctt aattttaag agatgtgtc  
 2041 gcaatgggtgc gctttataaa aaaaggctaa atgagggttgc tggccatgtc ggaatggatc  
 2101 tatactaaaa tacatggatg agaagggttgc ggtcaactgggtt cagatataatg aaaatttttta  
 2161 agatatcagg aggttttttataatgtt ttggctgcattt tcaaagatttt tttgcactca  
 2221 aagccaaaaaa aaaattttgtat tttaatttcat ggccttccat attcaggaaa gtcatttcat  
 2281 gcaatgtcat taataagggtt attaaaaggc agagtattat tttttgtaaa ttcaaaaaagc  
 2341 caattttgggt tgcaaccctt ttctgtatgtt aaaaatgtcat tgattgtatg tggtaactgtAC  
 E2 binding ->  
 2401 CCCTGTTGGT tatataatggaa taatttatcta agaaacgggt tagatggca ttatgtctca  
 2461 ttggattgtt aatacaaaaggc tccaaatgcac acaaagggttcc ctccatttattt actaacaatct  
 2521 aatataaaatg tgcatggatg agctaattac agataacttac acagtagaaat taaaggattt  
 2581 gcatttccaa atccattttccat aatgaaatca gacgatacac ctcagttgtc gttactgtac  
 2641 caaaggcttgc aatctttttt tggacacaat TAGaacttcac tgaccaagaa  
 E2 orf start ->  
 2701 gacgagggcg aaaATGgaga atctcagcga ggcgttcaat gctctgcagg atctgctaat  
 E2 cds ->  
 2761 gaacatttaT GAAGctgcag aacagacact tgaggcacag ataaaacact ggcaaaacctt  
 <- E1 end  
 2821 gcgacaagaa gctgttttgc tctactttgc taggcagaga ggtgtgacaa ggcttggata  
 2881 tcaacctgtc cctgtaaaaggc ctgtatctgtc agcggaaatgtt aaagaggcttca tagcaatgtt  
 2941 gctgcagctt cagtctctac aaacgtctgtc atatgtcatc gaaacttgc cattatgttgc  
 3001 caccagtata gaaacttttgc gaaaggctcc agacgggtcac tttaaaaagg gtcggatgt  
 3061 tgttagaagtgc atttatgtaca atgtatgtc gagaatgttgc taaaggccaga agtgggggtca atgagactgg  
 3121 cgtgttattat atgaaagacg atgtgtggca taaaggccaga agtgggggtca atgagactgg  
 3181 catatatttttgc ttacaaggaa cattttaaata ttactatgtt ctatgttgc acgatgtc  
 acgatgtc

## HPV36

3241 taaatatagt caaactggac aatgggaagT GAaagttaat aaggaaaactg tccttgccccc  
E4 orf start ->  
NH<sub>2</sub> terminus unknown

3301 tgtcaccaggc tccacccttc cagggcgcc aggaggacaa gcagacacaa acgcctcctc  
3361 caagacctcc accaccacca cagccaccgt tgactccacg accaagcagc tcaccacatc  
3421 agaacagcca caacaaaccg aaaccaaagg aagaaagtac ggacggaggc cctccagcag  
3481 gacaaggaga ccgcaaggca agcaaaggcg atcaagggcc agacaccgt cctctaggc  
3541 ccgatcgccg tccccgtccc ggtcccacac cccaaacct cggctcgcca ccacccggc  
3601 taggtcccccg tcgctcgcca agactgggtt ccagcgggta tcaaccagat cacgatccag  
3661 aagcacctct aagaaggggag gtagaaggcg gaggtcacgg tcaccatcca cctcctcctc  
3721 caccaccacc accaacaac ggtcacgat gccccccgaa accacagggt ccagaggggc  
3781 gcgaggggggt agagggggca ggggtggag cggtgggggg cggcgcacgag gacgatcatc  
3841 ctccctccacc tccccccccc acaaacggtc aagagagcac tctgttagga gccgtggcgt  
3901 gctcctgac caagtggaa agtcaactcg atctgttagt tcaaaacata caggacgact  
3961 tggaagatta ctggagaag ctctcgatcc cccagTGAtc ctgttagag gggaggc  
-< E4 end

4021 tacactaaaa tgcttcgca acagagctaa gataaaatac atggactgt ataggtcatt  
4081 tagtacaact tggtcatggg tggcaggaga tggcactgtg cgtctaggca gccccagaat  
4141 gctcatttagc ttttcgtcc acaatcagag aagggtttt gatgacgtgg tgagataccc  
4201 gaaaggagtt gaaaatcat atggcaaccc tgcacgtctc TAActaa tgctatgctg  
-< E2 end

4261 ctgtgtact aacaacacTA Acaaatttgc tttttatact tttttacttt tgtaacttgca  
L2 orf start ->

4321 ATGgcgcgtg ctaaaagggt caagcgagac tctgtAACAC atatatacca gacctgcaaa  
L2 cds ->

4381 caagcaggca catgcccccc ttagtgggtg AATAAAgtgg aacaacaac agttgctgac  
signal ->

4441 aatattttga aatatggcag tgctgggtc tttttgggtg gccttggcat tggttcggc  
4501 cgaggtactg ggggtgcac cgggtacgtg ccacttagtg aaggctctgg tatccgtgtc  
4561 ggaggtaccc ccacgggtgt aaggcctca ttagttctg aagcaattgg gccagtcgat  
4621 attttggcca ttgatacaat ttagtgcgtg gaggctacag catcgccgt gttcctctt  
4681 actgaatcca ctggacatca tttacttcca ggtgggtgg aaacaatagc tgaattcat  
4741 cctgttgctg aaggccatc agttgatacc cctgtggta ccacaagcac gggttccagt  
4801 gctgtttgg aagttgcctc agagctata cctccaacac gggtagaat ctcacgtaca  
4861 caatatcaca atccttcctt tcaatttattt acagaatcaa cacatgcaca gggtaaagc  
4921 tctcttgac atcacattt agtgcacatca gggccggg gacaagaat agggctgat  
4981 attactgtg aaattgaact tcaagaactt cctagtagat atactttga aaatgaagaa  
5041 ccaactccac ctagacgtac cagcacaccc ttacaggcca cacatgcac agtagacgg  
5101 agaggtgttt cttaactaa tagacgtcta gtacaggcagg tacatgttgc aaatcctttg  
5161 ttttaactc aaccctctcg attgtgcgt tttgttttggaaaatcctgc atttgaagaa  
5221 gaagttacaa atatatttg aatgtatgtt gatgttttggaaaatcctgc atttgaagaa  
5281 ttcttgatg tccaaacgggtt gggcgtccc caatattctt caactcctgc agggtatgt  
5341 agggtagta gattaggtac tcgtgcaccc attcgacgc ggtctgggtc acaaataagg  
5401 tcacagggtgc actttatag ggtatctcgt tccatataata ctgaagatcc tatagaattt  
5461 cagttgttgg ggcaacatcc gggggatgtc agtatagttc aaggccctgt gggaaagcaca  
5521 tttatagacg taaatgtgtc tgaaaatcct ttgtctgaaa gtgtggaaagc cttttctgt  
5581 gatttattgc tggatgaagc tggatggaggat tttagtgggtt cacaatttagt tattggtaat  
5641 agaagaagta ccacttcctt cactgttccc agatggaaa ctactaggag tggttcttat  
5701 tatgtccagg acagtaaagg atattatgtt gcatacccg aatctcgaa taatgcagaa  
5761 ataattttac ctacacctga tatACCTGTA GTGGTAAatc acactcATGtcaatacaggt  
E2 binding ->L1 orf start ->  
first 'ATG' of L1 cds ->

5821 gacttttatt tacatccttag tcttcgtatgg cgcaaaacgtt aaagaaaata ttgtTGAttt  
-< L2 end

```

5881 tgcattgcAG ATGgcagtgt ggcattcggc taatggtaaa gtatacccttc ctccatcgac
      /\ 3' sj
probable L1 ->
cds start
5941 accggttgcc agggtgcaaa gcacggatga atatatacaa aggacaataa tttattatca
6001 tgcattcagc gacagactac tgactgttagg ccatccatac ttcaatgttt acgatattac
6061 tggtaacaaa ttagaagtcc ctaaaagtgtc tggtaaccaa cacagggtt ttcgcttggaa
6121 attacctgat cctaatacgat ttgcatttagc tgacatgtca gtttataacc cagataaaga
6181 acgggttgtt tggagctgtt ggggccttga aataggtaga ggacaaccgt taggtgttgg
6241 cagtagggaa caccactat ttaataagtt gaaagacact gaaaacagta attcatatat
6301 aaaatcttct aaagatgata gacaggatac atcattttagt cccaaacaaa ttcaaatgtt
6361 ttcgtggga tgcacaccc tttaggtga acatgggac aaggctatac cttgtgaaaa
6421 ggagcgccag gacaacagac tatgcccacc aattgaattt aaaaactactt atatagaaga
6481 tggcgacatg gcagatatacg gttttggaaa tttaaacttc aaaaatctgc aagagagtag
6541 gtcagatgtt agtttggata tagttaatga aacctgcaaa tttctgact tttaaaaat
6601 gcagaatgtt gtttatggag atgcctgtt ttttatgtt cgccagagac aatgttatgc
6661 cagacatttt ttgtccgtt gaggtttttt ggggtgacgac atccctgacg ccagaatttga
6721 taatgggact tttaagaatc agttttcat tcctggggct gacggccaag atcaaaagac
6781 catagggaaat gccatgtatt accaaactgt tagtggctca ttgggtctca gtgatgctca
6841 attgttaaac aggccttct ggctccagcg agcacaaggc cataataatg gcattctgtt
6901 ggtaatcag atgtttttaa cagttgttca caacacacga aataactaact ttgttattt
6961 aatatataac aataatgggg cactaaagga catcaatgtat tacactgcag agcaatttag
7021 agaatatcaa aggcacgtgg aggaatatga aatttcatta atattacagc tatgttaagg
7081 tcctctgaag gcagaagttt tggctcagat aaatgttcatg aatttttctt tatttggaaaga
7141 ttggcagttt ggtttgtac ctactccaga taacccttta caagacacct atcgatatat
7201 tgatttcatta gccactcgct gtcctgtttaa aaccccccctt aaggaaaaag agatccctt
7261 caaggggtt aagttctggg atgtggatct tactgaacgg ttgttacttag atttggatca
7321 atactcttta ggttagaaat ttctatttca agccggctta cagcagacgA CCGTAAGCGG
                                         E2 binding ->
7381 Tacaaaatca gtgtcttatac gagggttcac cagaggaacc aagcgcaagc gaaaacagTA
7441 AtatgACCGT TTTTGGTaca gatttataaa cttttacaca gtattcaagg aatgtttgtt
      <- L1 cds
E2 binding ->
7501 tactctgact aagtataact ctaccaaggg aaccgACCGC ACCCGGTaca gtcaacgata
                                         E2 binding ->
7561 ctgctgccaa tataacttct gtttagtgcc agaacatatac atcttggaaag cagatcgacc
7621 gtgttcgttg taacacgctc ggatttagaga cattgccaag gaagatttaa tctacaatcg
7681 ctgttggcaa tcgctttgg ctgagatagc tgaccggtaa cg
//
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**HPV37**

LOCUS HPV37 7421 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 37, complete genome.  
ACCESSION U31786  
KEYWORDS .  
SOURCE Human papillomavirus type 37.  
REFERENCE 1 (bases 1 to 7421)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Scheurlen,W., Gissmann,L., Gross,G. and zur Hausen,H.  
TITLE Molecular cloning of two new HPV types (HPV 37 and HPV 38) from a  
keratoacanthoma and a malignant melanoma  
JOURNAL International Journal of Cancer 37 (4), 505-510 (1986)  
REFERENCE 3 (bases 1 to 7421)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV37, as well as HPV9, was found in a keratoacanthoma in a patient  
who also had a basaloma. The HPV37 DNA was present as a circular  
monomeric episome, with approximately 10 copies per diploid cell.  
HPV37 was not detected in the basaloma. Keratoacanthoma is "a  
rapidly growing benign skin tumor which originates from the hair  
follicle and may resolve spontaneously after a period of months.  
It grows invasively and occurs as a single lesion or as multiple  
tumors. Tumors are found preferentially in areas exposed to  
sunlight. This proliferation has been suspected to be of viral  
origin, but there exists as yet no evidence to support this  
concept." [2] HPV37 was not found in 231 other tumor DNAs  
originating from different tissues (including 6 keratoacanthomas and  
35 malignant melanomas, as well as 190 other tumors); thus no  
correlation has been found so far between HPV 37 and any tumors of  
the skin or other tissues. HPV-37 is closely related to HPV 9, 15,  
17, 22, 23, 38 by cross-hybridization as well as phylogenetic  
analysis. These types also have in common a relatively short (7.4  
kb) genome.  
BASE COUNT 2345 a 1343 c 1666 g 2067 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 agccaagaat atttggcaga acattttctt ggaagacaAC CGATAACGGT aagattgtaa  
E2 binding ->  
61 tcttcAACC GTAGGCGGTa ctttctgatt ggtttggccg atttagct acaacaatct  
E2 binding ->  
121 ttcttcAATA atacatgtaa ccgcctgcgt taacttacat gatctaaata aatatgtga  
E6 orf start ->  
181 gcaatactta agagaatata TGgttaggcc taaggctcaa tctgtcaac agcttgcaga  
E6 cds ->  
241 tactttatgt atacctttag tagatgtttt actgccttc agattttgtt atagattctt  
301 agcatatata gaatttgatcg catttgatcg aaaaggtctt caactaattt ggaccgaaga  
361 agattttagt tatgcgtgt gtactagctg tgcctatgtc acagcacagt ttgaatttac  
421 cagtttctat gggacttcg ttagtggag ggagatagaa gagatagacaaaagccat  
481 aggagaaata gccatacgt gcaaattttt cttaaagttt ttggatttgt tagagaagtt  
541 ggagacttgc tatactcagc aacaatttca caaggtttagg cgcaatttggaa aaggcttgcgt  
601 TAGacattgt gggtcgatag gATGAtttggg aaagaagcta caataccaga aatagtgcctt  
E7 orf start -> <- E6 end  
E7 cds ->  
661 gagctgcaag agcttgcata gcccactgct gacctgcatt gttacgaaga gttgagtgaa



## HPV37

3781 cccagTAAt tgcgtgcgt ggtgatgcta acaaattaaa atgctatcgc tatagagcta  
    <- E4 end  
3841 agaaaaagca tggaaaccta gttaagtact acagtaccac gtggcatgg gttggggca  
3901 gcaccaatga tagaatttgg aagtcacgca tgtaatgc attcaatcc aatacagaaa  
3961 gagagttgtt tttaaaaact atgaaattac caccagggt tgattgtca ctgggtcatt  
4021 tagatgaatt gTGAAaacag ctttttata acaaactaac attgcttttgccttgctac  
    <- E2 end  
4081 TAAcctacta acgttccaAT Ggctcgca cgctgtacca aacgtgcgtc tctaactgac  
L2 orf start -> L2 cds ->  
4141 atttacaggg gttcaagca ggccggcact tgcccccccg atgtattAA TAAAgtggaa  
    signal ->  
4201 caaacaacaa ttgcagacaa aatttgaag tatgggtgt ctgggtttt ttttgtgg  
4261 ctgggatta gcacccggc aggAACAGGT ggtgtacag gatatgtccc ttgggggaa  
4321 gcccctggag tgcgttagg aggccaccc accattgttcc gccctgggt catacctgaa  
4381 ttgattggc cagcagatgt aatacctatt gacacagtca ctccaattga ccccgagca  
4441 cccagtattt tcacaattac agacagttagt gctgttgacc tttacctaa tgaatagaa  
4501 acaatttgcag aagtgcattc tgcgttccaca gacaatttgg atattgatac tcctgttagt  
4561 acaggaggcc gggattccag cgctgttttgaagttgtc atcctagtcc ccctgtgcga  
4621 acaagagttt ccagaacaca atatcataat cttcttttca aaataataac tgaatctaca  
4681 cctttagcag gagaatctgc tttagctgac catgttattt ttttgaagg cactggagga  
4741 caaaatatag gtggttctcg aaatgcact atagaaacag ctcaagaaag ttttgaatg  
4801 caaagttggc cgagtagta tagtttggaa atagaagaag gaacacctcc tagatctagc  
4861 acaccagtac aaagagcagt acaatcactc tctagttaa gacggcatt gtataatagg  
4921 agattaacag aacaggtac agtcacggat ccttatttc tgtagtagacc ctcacaatta  
4981 gtacagtttc agtttgcacaa tcctgcattt gaagaagaag taactcaaattt atttggagg  
5041 gatTTTgagg ctgtagaaga acctccagat agacgtttt tggatgttat tcgcttaggt  
5101 agacctactg ttgcgttac accacaagcg tatttaagag taagcagatt aggacgtcg  
5161 gctaccatcc gtactcgttag tggcacag gtggggcgtc aggtacattt ttatagagat  
5221 ttaagtacta tagattctga tgccttagaa atgcaattat taggagaaca ttcaggtgat  
5281 actactatag tacaaggacc tgcgtttagt tcattgtttt atataaatat tgcgttacca  
5341 ggtcccttaa atataggcaca acaagagtct actatggcag atgacacaga ttttattct  
5401 gcagattttt tgtagagga tgctgttagaa gacttctcag gatctcgtt ggttttgg  
5461 acctcacgccc gcagtacaaa ttctatcaca ataccttagt ttgaaactcc aagagatact  
5521 ggattttata tacaagatata tcaagggtac aatgttagctt atcctgatgc acgtgacaca  
5581 acacaagttt tcttgccaca acctgaaaca ccaactgttag ttatttagatt tggagaggca  
5641 ggtacagact attatttaca tcctagctt aaaaagaaaa agagaaaacg caaatattta  
5701 TAAttgttt tacagATGac tttgtggctg ccagcgacgg gtaaagtata ctgcctcca  
    <- L2 end  
L1 orf start -> L1 cds ->  
5761 acaccaccag tagccgggt gcaaaacgcg gatgattatg tggaaagaac aaatgtattc  
5821 tatcatgcca tgacgcgtcg tctcttaact gtggacacc catattatga tgcgttac  
5881 agtgatggct taaaatcga ggttctaaa gttatggaa atcaatacag agcttttag  
5941 gtaggttgc cagatccaaa taaatttgc ttagcagata tgtagtata taatccagaa  
6001 aaggaaaggt tgggtggc ctgtggcc ttggagatag gccgagggca accacttgg  
6061 gtaggaacga caggtcaccc ttatattaaat aatattttttt aactttaggg acacttgg  
6121 tACCAAGGGGG GGTcacggga tgatagacaa aacacatcat ttgtatccaaa acaagtacag  
E2 binding ->  
6181 atgtttgttgg ttggatgtgt gccatgcgt ggtgaacatt gggataaagc accagttgt  
6241 gcatcagagg aaaataatca gacaggacag tgcgttccaccat tttttttttttaaaa  
6301 attgaagatg gggacatgtt tgatataggg ttccggaaata ttaacaataa ggttctct  
6361 actaataat cagatgttag tttagatata gtaatggaaa tatgcacataa ccctgatttt  
6421 ttaacaatgg ctaatgtgtt ttatggggat gcatgtttct tttttgttag gagagaacaa  
6481 tgcgttgcac gacattttt tgtaagaggg gaaatgttag gtgtatgtat tcccgatgg  
6541 actgttaatc aggaccacaa atattactt cctgcacaaat cagaccacgc gcaatct  
6601 ttggcaatt ctacctattt tccactgtt agtggatctt tagtaacatc tgatgtcg  
6661 ctctttaaca ggccttttgc gttacgcaga gctcaagggtc acaacaatgg cattttatgg  
6721 ggtatcaaa tgtttatcac agttgtgtat aatacaccggaa acacaaactt ttcttattgt  
6781 gttgtctactg acaatggcga agttacagaa tataattctc aaacactcg agaataccta  
6841 agacatgttgg aagaatacca gcttcaattt attttacaaac ttgttaaagt tcctttaaag

6901 gctgagggttt taactcagat aaatgcaatg aattctggta tattggaaga gtggcaatta  
6961 ggatttgtac ctactccaga taattcagta catgACCTTT ATAGGTacat taattcaaag  
E2 binding ->  
7021 gctaccaagt gtcctgatgc agttgtgaa aaagaaaaagg aagatccctt tgcaaaaatat  
7081 acattttggaa atgttagattt aactaaaaaa ttatcatttg atttagatca atatcctta  
7141 gggagggaaat tcatcttca gtcgggattt caaagtagac ctagaattgt tcgatcgct  
7201 gtaaaaagtgt ctaaaggtaaa aaagcgtaaa cggtcgTGAC CGTTTCGGT ttccAATAAA  
<- L1 end signal ->  
E2 binding ->  
7261 caAATAAAcc aataaggtat gtgaagcatt tttaccatg ttcgtgacta aaccatataa  
signal ->  
7321 gtcAACGCCa acaACCGCAC CCGGTttaat cagatataaaa acacctggtg cgattttatc  
E2 binding ->  
7381 agagcttttg tggaagcacc tgaggcgacc gccagaactg c  
//

**HPV38**

LOCUS HPV38 7400 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 38, complete genome.  
ACCESSION U31787  
KEYWORDS .  
SOURCE Human papillomavirus type 38.  
REFERENCE 1 (bases 1 to 7400)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Scheurlen,W., Gissmann,L., Gross,G. and zur Hausen,H.  
TITLE Molecular cloning of two new HPV types (HPV 37 and HPV 38) from a  
keratoacanthoma and a malignant melanoma  
JOURNAL International Journal of Cancer 37 (4), 505-510 (1986)  
REFERENCE 3 (bases 1 to 7400)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV-38, as well as HPV17a, was found found in high copy numbers in  
a superficial spreading malignant melanoma of an immunosuppressed  
patient. The HPV38 DNA was present as a circular monomeric episome,  
with approximately 50-100 copies per diploid cell. Superficial  
spreading malignant melanoma is a tumor derived from  
pigment-producing cells of the skin with rapid invasive growth and  
high incidence of metastasis. Tumors are found preferentially in  
areas exposed to sunlight. HPV38 was not found in DNA from 231  
other tumors originating from different tissues, including 6  
keratoacanthomas and 35 malignant melanomas, as well as 190 other  
tumors. Thus, no correlation has been found so far between HPV 38  
and any tumors of the skin or other tissues. HPV-38 is closely  
related to HPV 9, 15, 17, 22, 23, 37 by cross-hybridization as well  
as phylogenetic analysis. These types also have in common a  
relatively short (7.4 kb) genome.  
BASE COUNT 2305 a 1383 c 1625 g 2087 t  
ORIGIN 200 bp upstream from beginning of E6 cds  
1 catctttggc agacgaagtg cACCGATAAC GGTaaagactt ttctctttta accgtaggcg  
E2 binding ->  
61 ttggtttatt attcctggca acaatggtgg ttaacaacca tcacacgtaa tcggtaacaag  
121 caACCGCTTG TGGTagtaaa atgaattaaa aaaaaaaaaaca aggatatatt taaggggcct  
E2 binding ->  
181 gTAAgcttgg gatgtattcA TGgaactacc aaaacctcaa actgtgcagc agctcaigtga  
E6 orf start -> E6 cds ->  
241 taagttaaca gttcctgttag aggatctgtt attaccctgt agattctgca acagttccct  
301 cacgtacatt gaattacgtg agtttgatta caagaactta cagttaatct ggactcaaga  
361 ggattttgtt tttgcatttt gtgcgcgtt tgcttatgct tctgctcaat atgaatgtca  
421 gcagtttat gaattaaactg tcttggccg tggaaattgaa caggtggagc aacagacaat  
481 aggccttatt gttataaggt gtcagtattg tttaaaagtgt ctgtattga tagaaaaatt  
541 agatatctgt tgctctcatc aagcatttca caaggTAGa ggcaattgga aaggaaggtg  
E7 orf start ->  
601 caggcattgc aaagcaatag aATGAtttggg aaacaagcta ctcttcgtga tatagttctt  
<- E6 end  
E7 cds ->  
661 gaagagcttg tccagcccat tgacctgcat tgccacgagg agttgcctga tcttccagag  
721 gatattgaag catcagtggt agaggaggag ccagcataaca ccccatacaa aatcatagtt  
781 ctttgtgggg gttgtgaagt aaggctaaaa ctatacgtgt gggccaccga cgctggatt



HPV38

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6961 aagcaactaa atgtccagat gcagtgccctg aaacagaaaaa agaagatccc tttggtaat
7021 atacattttg gaatgtggac atgactgaaa aattgtctct agatttggat caatatcctt
7081 tggggcgcaa atttttattc caaggcagggt tacaaacgc acgaacacgt gctgtcaaac
7141 ggccgttagt aagaaaaatct tccaaatctg taaaacgcaa aaggaccagg TAACCGTTTT
                                         <- L1 end
                                         E2 binding ->
7201 CGGTcgccccA ATAAAattta ttaactaatg tggtatgtga agcattttt gaccttcttt
      signal ->
7261 gtgactaaac cgaacaagtc aacaccagta ACCGCGCCCG GTtaatcaga ttataaaattc
                                         E2 binding ->
7321 ctgaagggca gattcaatc agtgcagata tcatctagca cctgcagcaa ccgccaagac
7381 tttgcagga cttggcagaa

//
```

**ICPX1**

LOCUS HPVICPX1 276 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (ICPX1) L1 gene, partial  
cds.  
ACCESSION L38914  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (ICPX1) (individual\_isolate  
Kremsdorf et al.) DNA.  
REFERENCE 1 (bases 1 to 276)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeer,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
JOURNAL J. Clin. Microbiol. 33 (3), 690-695 (1995)  
MEDLINE 95270695  
COMMENT HPVICPX1 was isolated from an immunocompetent patient [1],  
and is likely to constitute a new HPV type. The most closely  
related known type appears to be HPV-8.  
NCBI gi: 623453  
BASE COUNT 91 a 51 c 54 g 80 t  
ORIGIN  
1 atttcggttt atagtgaagg tggacaaata aaagatatac gggactacac atctacacag  
L1 cds ->  
61 ttcaaggaaat atttaaggca tgtggaggaa tatgaaaatat ctgtcatatt gcagttatgt  
121 aaaatacctt taaaagcaga agtcttggtc cagataaaatg ccatgaaccc ctattatttg  
181 gaggactggc aatttaggatt tgtccctaca cctgacaatc caattcatga tacctacaga  
241 tttagtgact ctttggctac ccgatgccct gacaaa  
L1 cds ->  
//

LOCUS HPVRTRX1 267 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX1) L1 gene, partial  
cds.  
ACCESSION L38918  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX1) DNA.  
REFERENCE 1 (bases 1 to 267)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeer,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
J. Clin. Microbiol. 33 (3), 690-695 (1995)  
JOURNAL 95270695  
MEDLINE  
COMMENT HPVRTRX1 was isolated from renal transplant patients [1],  
and is likely to constitute a new HPV type. It was isolated  
during a search for HPV DNA in 5 out of 53 squamous cell  
carcinomas from 2 of 26 renal transplant patients. The most  
closely related known HPV types appear to be HPVs 22, 23, and  
38. The partial L1 sequences for HPV42 and HPV73 do not  
overlap with that of HPVRTRX1; from their similarity to  
HPVs 22, 23 and 38, it is possible that HPVRTRX1 and one of the  
other two isolates are from the same novel HPV type.  
NCBI gi: 623461  
BASE COUNT 98 a 41 c 52 g 76 t  
ORIGIN  
1 atcagtgtta ctagtgaaga tttaagtaca gcaaaatatg atgctaaaaa tatcaggaa  
L1 cds ->  
61 tatatgagac atgtagaaga atatcaatta tcatttat tacagttatg tagggtaccc  
121 ttagaggctg aggtgctaac ccagattaat gctatgaatt caggtatatt agaaaactgg  
181 caactagggt ttgttccaac accagataat gcagtgcattt acacatatcg ttaccttagt  
241 tcaaaagcta caaaatgtcc agatgca  
L1 cds ->  
//

## RTRX2

LOCUS HPVRTRX2 276 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX2) L1 gene, partial  
cds.  
ACCESSION L38919  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX2) DNA.  
REFERENCE 1 (bases 1 to 276)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeer,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
J. Clin. Microbiol. 33 (3), 690-695 (1995)  
JOURNAL 95270695  
MEDLINE  
COMMENT HPVRTRX2 was isolated from renal transplant patients [1],  
and is likely to constitute a new HPV type. It was isolated  
during a search for HPV DNA in 2 out of 53 squamous cell  
carcinomas from 2 of 26 renal transplant patients. The most  
closely related known HPV types appear to be HPVs 22, 23, and  
38. Although clearly more closely related to EV-associated types  
than to other HPV types, it is not particularly closely related  
to any known types, but it does appear to be more closely related  
to the novel sequences for HPVRTRX4 and HPVRTRX5.  
NCBI gi: 623463  
BASE COUNT 99 a 50 c 53 g 74 t  
ORIGIN  
1 atagctgttt atcaggaaca gaagaaggta aaagaaaatag agagttacga ttctaccaag  
L1 cds ->  
61 tttaatgaat tccaaaggca tggtgaagaa tatgaagtat cacttatttt acagctttgt  
121 aaaattccac taaaggctga ggtgctagcc aaaattaatg caatgaactc tgacattctg  
181 gagaattggc agttaggggtt cgtacacctaca ccagataatc ctattcacga cacatacaga  
241 tatttagact ctttggccac acgctgccccaa gaaaaaa  
L1 cds ->  
//

LOCUS HPVRTRX3 267 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX3) L1 gene, partial  
cds.  
ACCESSION L38920  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX3) DNA.  
REFERENCE 1 (bases 1 to 267)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeier,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
JOURNAL J. Clin. Microbiol. 33 (3), 690-695 (1995)  
MEDLINE 95270695  
COMMENT HPVRTRX3 was isolated from a renal transplant patient [1],  
and is likely to constitute a new HPV type. It was isolated  
once during a search for HPV DNA in 53 squamous cell carcinomas  
from 26 renal transplant patients. The most closely related  
known type appears to be HPV-9. The partial L1 sequence for  
HPVVS92 does not overlap with that of HPVRTRX3; from their  
similarity to HPV-9, it is possible that HPVRTRX3 and HPVVS92  
are from the same novel HPV type.  
NCBI gi: 623465  
BASE COUNT 90 a 45 c 50 g 82 t  
ORIGIN  
1 attagtgtcg ccacagatgc aggtgtaact actgaatatac aggctaatac aatcagagaa  
L1 cds ->  
61 tatttaagac atgttgagga atatcaacta tctctcattt tacaactctg taaagtacct  
121 ttaaaggctg aggtattaac tcagatcaat gcaatgaatt ctggtagttt agaggactgg  
181 cagttaggct ttgtgcctac agcagataat tcagtagatg atatttacag atatattaat  
241 tcttagagcca caaaaatgtcc agatgct  
L1 cds ->  
//

## RTRX4

LOCUS HPVRTRX4 276 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX4) L1 gene, partial  
cds.  
ACCESSION L38921  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX4) DNA.  
REFERENCE 1 (bases 1 to 276)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeer,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
JOURNAL J. Clin. Microbiol. 33 (3), 690-695 (1995)  
MEDLINE 95270695  
COMMENT HPVRTRX4 was isolated from a renal transplant patient [1],  
and is likely to constitute a new HPV type. It was isolated  
once during a search for HPV DNA of 53 squamous cell carcinomas  
from 26 renal transplant patients. The most closely  
related known HPV types appear to be HPVs 22, 23, and 38.  
Although clearly more closely related to EV-associated  
types than to other HPV types, it is not particularly  
closely related to any known types, but it does appear to  
be more closely related to the novel sequences for HPVRTRX2 and  
HPVRTRX5.  
NCBI gi: 623467  
BASE COUNT 89 a 51 c 48 g 88 t  
ORIGIN  
1 attgctgttt acaatgaagc aggtaaaata caggatattt ctcatatga ttctacaaaa  
L1 cds ->  
61 tttagagaat ttcaaaggca cgtagaggaa tatgaagttt cttaatttt acaactatgt  
121 aagattcctc taaaggctga ggtgctggcc caaatcaatg ctatgaatcc atctatTTA  
181 gaagattggc aattgggctt tgtacctaca ccagacaatc ctattcatga tcgttatcgc  
241 tacatagatt cttagccac tcgatgtccc gaaaaa  
L1 cds ->  
//

LOCUS HPVRTRX5 276 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX5) L1 gene, partial  
cds.  
ACCESSION L38922  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX5) DNA.  
REFERENCE 1 (bases 1 to 276)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeier,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
J. Clin. Microbiol. 33 (3), 690-695 (1995)  
JOURNAL 95270695  
MEDLINE  
COMMENT HPVRTRX5 was isolated from renal transplant patients [1],  
and is likely to constitute a new HPV type. It was isolated  
during a search for HPV DNA in 2 out of 53 squamous cell  
carcinomas from 2 of 26 renal transplant patients. The most  
closely related known HPV types appear to be HPVs 22, 23, and  
38. Although clearly more closely related to EV-associated types  
than to other HPV types, it is not particularly closely related  
to any known types, but it does appear to be more closely related  
to the novel sequences for HPVRTRX2 and HPVRTRX4.  
NCBI gi: 623469  
BASE COUNT 91 a 42 c 49 g 94 t  
ORIGIN  
1 atagcagttt ataatgattc tggtaaaatt aaagacattg cttcttatga ttccactaaa  
L1 cds ->  
61 ttgcgagagt ttcaaagaca tgtgaaagaa tatgagatt cttaatttt acagttatgc  
121 aaaattccctt taaaatcaga ggtatttagct caaattaatg ctatgaatcc tacaatactt  
181 gaggattggc aatttagttt tgtgccaact cctgataatc caatacagga tgcttacaga  
241 tatttggatt ctttggctac acggtgccca gataaa  
L1 cds ->  
//

## RTRX6

LOCUS HPVRTRX6 267 bp DNA VRL 13-JAN-1995  
DEFINITION Human papillomavirus unidentified type (RTRX6) L1 gene, partial  
cds.  
ACCESSION L38923  
KEYWORDS L1 gene.  
SOURCE Human papillomavirus unidentified type (RTRX6) DNA.  
REFERENCE 1 (bases 1 to 267)  
AUTHORS Berkhout,R.J., Tieben,L.M., Smits,H.L., Bavinck,J.N., Vermeer,B.J.  
and ter Schegget,J.  
TITLE Nested PCR approach for detection and typing of epidermodysplasia  
verruciformis-associated human papillomavirus types in cutaneous  
cancers from renal transplant recipients  
JOURNAL J. Clin. Microbiol. 33 (3), 690-695 (1995)  
MEDLINE 95270695  
COMMENT HPVRTRX6 was isolated from a renal transplant patient [1],  
and is likely to constitute a new HPV type. It was isolated  
once during a search for HPV DNA in 53 squamous cell carcinomas  
from 26 renal transplant patients. Although clearly more  
closely related to EV-associated types than to other HPV types,  
HPVRTRX6 constitutes a relatively isolated sequence.  
NCBI gi: 623471  
BASE COUNT 89 a 46 c 52 g 80 t  
ORIGIN  
1 atttgtgtac cttagatgc aggtgctgta actgagttatg attcttagcaa atttagagaa  
L1 cds ->  
61 tttttaaggc acgtggaga gtatcaaata tctgttaatat tacaactgtg taaagtatca  
121 ctgcaacctg atgtgctagc ccagatcaat gcaatgaatt caggtatatt agaagattgg  
181 cagtttagat ttgtaccaac tcctgacaat gcagtacatg acacctatacg atttataaat  
241 tcctcagcca ctaaatgtcc agataag  
L1 cds ->  
//

LOCUS HPVTogawa 395 bp ds-DNA VRL 10-DEC-1994  
DEFINITION Human papillomavirus L1 gene fragment.  
ACCESSION L38388  
SOURCE Human papillomavirus DNA.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS Togawa,K. and Rustgi,A.K.  
TITLE A novel human papillomavirus sequence based on L1 general primers  
JOURNAL Virus Res. 36, 293-297 (1995)  
COMMENT Togawa et al (Gastroenterology 107:128-36, 1994) identified an HPV strain with a novel restriction digest pattern in 14% of squamous cell carcinomas. Sequence of a fragment of the L1 gene indicates that this sequence is related to HPV-types associated with EV. The most closely related known HPV types appear to be HPVs 22, 23 and 38. The partial L1 sequences for HPVVS42 and HPVVS73 do not overlap with that of the Togawa isolate; from their similarity to HPVs 22, 23 and 38, it is possible that the Togawa strain and one of the other two isolates are from the same HPV type.  
NCBI gi: 598358  
BASE COUNT 137 a 60 c 76 g 122 t  
ORIGIN  
1 gatactacac gcagtactaa ttttagtatac agtgttaaaa atgaggatag cttagcaaat  
61 tataatgcta gaaatattag agaatacatg agacatgtt aggagtatca gttgtcttt  
121 atattacaat tgtcagaat acctttaaaag gctgaggtt taacacaaat caatgcattg  
181 aactctgata ttttagagaa ttggcaattt ggctttgtac ctacaccaga taatgcagta  
241 cacgatacat ataggtattt agcctaaaaa gccactaagt gtcctgatgc agtacacctgaa  
301 accaaaaaag aagatccccc tggaaaagtat tcattctgga atgttgatat gacagaaaaaa  
361 ttgtcgctag atttagatca gtttcctttt ggacg  
//

# HPV75L1

LOCUS HPV75L1 661 bp DNA VRL 15-NOV-1994  
DEFINITION Human Papillomavirus type 75 ds-DNA, part of L1 ORF.  
ACCESSION X79942  
KEYWORDS capsid protein; L1 gene.  
SOURCE Human papillomavirus.  
REFERENCE 1 (bases 1 to 661)  
AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur Hausen,H. and de Villiers,E.M.  
TITLE Specific types of human papillomavirus found in benign proliferations and carcinomas of the skin in immunosuppressed patients  
JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
MEDLINE 94340583  
REFERENCE 2 (bases 1 to 661)  
AUTHORS Shamanin,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld 242, 69120 Heidelberg, FRG  
COMMENT HPV-75 (VS40) was isolated from a dysplastic art biopsy of a renal allograft patient, and is likely to constitute a new type. It was found in a search for HPV DNA in 118 skin lesions taken from 46 renal allograft patients [1]. HPV-49 appears to be the most closely related known type.  
NCBI gi: 562314  
BASE COUNT 195 a 118 c 155 g 193 t  
ORIGIN  
1 tctagggggc aacccttggg ggttagttct acaggccatc ctttggtaaa taaagtaaag  
L1 cds ->  
61 gatactgaaa attcaaataa ttatataaca atgtctaaag atgataggca ggacaccccg  
121 ttggacccta agcaggttca aatgtttatt attggctgtg caccttgtat agggggagcac  
181 tgggatgctg ccaaaccctg tgacgctgac aaaggagacg gttaatgtcc accttttagaa  
241 ttagtaataa cagttattga ggatggggat atggtgata taggtttgg taacataaat  
301 aataaaaacctt tgcgcgaaa taaatcagat gtcagttgg atatagttaa taacatttgc  
361 aagtatccag acttccttaa aatggccat gacatatatg gggactcctg ttttttttat  
421 gccaggcggg aacaatgtta tgctagacac tttttgtta gggaggca tgtaggcgt  
481 cgaattccta atgctgcagt gggtcaggac aataattttt tgttacctgc agccgctggg  
541 caggctcaaa acactttggg caactctatt tatgttccca cggtcagtgg ttctttgggt  
601 tccacagatg ctcaatttatt taacaggcca ttttggctgc aacgagcaca aggtcacaac  
661 a  
L1 cds ->  
//

**HPV76L1**

LOCUS HPV76L1 668 bp DNA VRL 15-NOV-1994  
DEFINITION Human Papillomavirus type 76 DNA, part of L1 ORF.  
ACCESSION X79948  
KEYWORDS capsid protein; L1 gene.  
SOURCE Human papillomavirus.  
REFERENCE 1 (bases 1 to 668)  
AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur  
Hausen,H. and de Villiers,E.M.  
TITLE Specific types of human papillomavirus found in benign  
proliferations and carcinomas of the skin in immunosuppressed  
patients  
JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
MEDLINE 94340583  
REFERENCE 2 (bases 1 to 668)  
AUTHORS Shamanin,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld  
242, 69120 Heidelberg, FRG  
COMMENT HPV-76 (CR148) was isolated from a skin wart biopsy of a renal  
allograft patient, and is likely to constitute a new type.  
It was found in a search for HPV DNA in 118 skin lesions  
taken from 46 renal allograft patients [1]. HPV-49  
appears to be the most closely related known type.  
NCBI gi: 562308  
BASE COUNT 203 a 110 c 158 g 197 t  
ORIGIN  
1 tcaagaggac acccattagg agtagggtct acaggtcatc ccctattaa taaagtgaag  
L1 cds ->  
61 gatacgaaa atgctaataa ttatatagtt acatctaagg atgataggca ggacacctca  
121 tttgatccta aacaggttca aatgtttatt attggctgcg caccgtgcatt aggtgagcac  
181 tggatgcag ccaaggccctg tgatgctgac agaggggttag gcaaattgtcc acctttggaa  
241 ctggtaataa ctgtaataga agatggagat atggtgata taggtttgg aaatataat  
301 aataaaaaccc tgcagcaaa taagtcagat gtcagtttag atatagttaa taatatttgt  
361 aagtatccag actttttaaa aatggccat gacatatatg gagactcctg ttttttttat  
421 gctagacggg agcaatgtt a gcttagacat tttttgtt a gaggaggtaa tgtaggagat  
481 gctattcctg atgctgcagt gggtcaggac aataactttg tgttgcctgc agctgttggaa  
541 caggccccaaa acactttggg tagctctatt tacgtgccta ccgttagtgg ttctttggta  
601 tccacagatg cacaattatt taataggccc ttttggctac aacgagcaca gggtcataat  
661 aacggtat  
L1 cds ->  
//

**HPVVS20**

LOCUS HPVVS20L1 677 bp DNA VRL 15-NOV-1994  
DEFINITION Human Papillomavirus vs20-4 DNA, part of L1 ORF.  
ACCESSION X79941  
KEYWORDS capsid protein; L1 gene.  
SOURCE Human papillomavirus.  
REFERENCE 1 (bases 1 to 677)  
AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur Hausen,H. and de Villiers,E.M.  
TITLE Specific types of human papillomavirus found in benign proliferations and carcinomas of the skin in immunosuppressed patients  
JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
MEDLINE 94340583  
REFERENCE 2 (bases 1 to 677)  
AUTHORS Shamanin,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld 242, 69120 Heidelberg, FRG  
COMMENT HPVVS20 was isolated from a skin wart biopsy of a renal allograft patient. It was found in a search for HPV DNA in 118 skin lesions taken from 46 renal allograft patients [1]. HPV-24 appears to be the most closely related known type.  
NCBI gi: 562312  
BASE COUNT 225 a 115 c 145 g 192 t  
ORIGIN  
1 ggaagtggac aaccattagg cataggcagc agtggtcacc ctctgttaa caaggtaaat  
L1 cds ->  
61 gatacagaaa atggcaacac atataaaggg acaactaaag atgatagaca aaacattca  
121 ttgtgatcta aacaattaca gatgtttata attggctgtt caccatgtat tggtaacat  
181 tgggataagg ctccctgcatt tgtaatgtt attcaacaag gtagttgcc accaatagaa  
241 ttagttaaca catacatata gggtgagat atggctgtata taggatatgg caatctaaat  
301 tttaaagctt tacagaaaa tagatcagat gttagcttgg atattttaga tggaaatatgc  
361 aaatatccctg acttttacg aatgcaaaat gatgtatatg gcgatgcctg ttttttttat  
421 gctcgacggg agcaatgtt tgccaggcac tttttgtgc gtggggcaa acctgggtat  
481 gatatacctg gtgcccaat tgatgcaggg tcacataaaa atgaatatta catacaggca  
541 gcttcagacc aatcacaaaa tagttgggg aattctatgt atttcccaac tatcagtggc  
601 tcatttagttt caagtgtatgc tcaattattt aataggccct tctggctaca gcgagcacaa  
661 ggccaaaaca acgggat  
L1 cds ->  
//

LOCUS HPVVS42L1 665 bp DNA VRL 15-NOV-1994  
 DEFINITION Human Papillomavirus vs42-1 DNA, part of L1 ORF.  
 ACCESSION X79943  
 KEYWORDS capsid protein; L1 gene.  
 SOURCE Human papillomavirus.  
 REFERENCE 1 (bases 1 to 665)  
 AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur  
 Hausen,H. and de Villiers,E.M.  
 TITLE Specific types of human papillomavirus found in benign  
 proliferations and carcinomas of the skin in immunosuppressed  
 patients  
 JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
 MEDLINE 94340583  
 REFERENCE 2 (bases 1 to 665)  
 AUTHORS Shamanin,V.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
 Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld  
 242, 69120 Heidelberg, FRG  
 COMMENT HPVVS42 was isolated from a verrucous biopsy of a renal allograft  
 patient. It was found in a search for HPV DNA in 118 skin  
 lesions taken from 46 renal allograft patients [1]. HPV-22  
 HPV-23 and HPV-38 appear to be the most closely related known  
 types. The partial L1 sequences for the Togawa sequence  
 and HPVRTTRX1 do not overlap with that of HPVVS42; from their  
 similarity to HPVs 22, 23 and 38, it is possible that HPVVS42  
 and one of the other two isolates are from the same HPV type.  
 NCBI gi: 562316  
 BASE COUNT 206 a 104 c 146 g 209 t  
 ORIGIN  
   1 ggttagggggc aaccatttgg ggttaggcact acaggtcatc cattatttaa caaattacgt  
   L1 cds ->  
   61 gatgcagaaa attccagcga acgtcaggga gatactgctg cagatgacag aatgaatata  
   121 tcttttgcataa ctaaggcggt acaaatgttc ataatacggtt gcacaccgtt tttaggtgaa  
   181 tattgggatc aaggccctgt atgtaaagat gcaggttaacc aaatgggctt atgtcctcct  
   241 ctgaaactaa agaatgtgt catagaagat ggagatatgt ttgatataagg ctggtaaac  
   301 attaataata agacactgtc attcaataga tcagatgtt gttagatat tgaaatgaa  
   361 atatgcaaattt atccagattt tttaacaatgt tccaatgtt gttagatat tgaaatgaa  
   421 ttttgtgctc gaagagagca atgttatgtc agacattattt ttgtacgagg cgtgttttt  
   481 ggagattcta taccagacgg tgcaatccat cagactaaca aatattattt agttcagct  
   541 caaaataata gcttgaaaa ttctacatat ttcccaactg taagtggttc tttagtgact  
   601 tctgatgctc agctatttaa cagaccctt tggtaaagc gtgctcaagg gcataataat  
   661 ggaat  
   L1 cds ->  
 //

**HPVVS73**

LOCUS HPVS73L1 612 bp DNA VRL 21-NOV-1994  
DEFINITION Human Papillomavirus vs73-1 DNA, part of L1 ORF.  
ACCESSION X79944  
KEYWORDS capsid protein; L1 gene.  
SOURCE Human papillomavirus.  
REFERENCE 1 (bases 1 to 612)  
AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur Hausen,H. and de Villiers,E.M.  
TITLE Specific types of human papillomavirus found in benign proliferations and carcinomas of the skin in immunosuppressed patients  
JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
MEDLINE 94340583  
REFERENCE 2 (bases 1 to 612)  
AUTHORS Shamanin,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld 242, 69120 Heidelberg, FRG  
COMMENT HPVVS73 was isolated from a skin wart biopsy of a renal allograft patient. It was found in a search for HPV DNA in 118 skin lesions taken from 46 renal allograft patients [1]. HPV-22, HPV-23 and HPV-38 appear to be the most closely related known types. The partial L1 sequences for the Togawa sequence and HPV-RTRX1 do not overlap with that of HPVVS73; from their similarity to HPVs 22, 23 and 38, it is possible that HPVVS73 and one of the other two isolates are from the same type.

NCBI gi: 562307

BASE COUNT 193 a 98 c 131 g 190 t

ORIGIN

1 taaacttaga gattcagaaa attctgcaga acgtctggaa ggaacaagtg atgataggag  
L1 cds ->  
61 gaatatataca tttgatccta agcaagtgc aatgtttgtg ataggctgca ccccctgtt  
121 agggaggtat tgggatacag ctccagttatg taaagatgca ggaagtcaat taggccttt  
181 ccctccatta gaattaaaaa acagtgttat agaagatggc gatatgttg atataggatt  
241 tggcaatatt aacaacaaaa cattaagttt taataagtc gatgttagtg tgacattgt  
301 taatgaaatt tggaaatatac ctgatTTTT aactatgtcc aatgtatgtt atggagactc  
361 ttgcttttc ttgctcgca gagagcgatg ttatgcaagg cattatTTT tacgcggagg  
421 ggcagtgggt gatttaatac cagatgctac agttaatcag gaccataaat attacttacc  
481 agcaaatcca cctgccacat tggaaaactc tacataactt ccgactgcta gtggctcctt  
541 agtgacatct gatgcacaat tatttaatag gccctttgg ttaaaacgtg cacaagggtca  
601 taataatggat

L1 cds -&gt;

//

LOCUS HPVVS75L1 686 bp DNA VRL 15-NOV-1994  
 DEFINITION Human Papillomavirus vs75-3 DNA, part of L1 ORF.  
 ACCESSION X79945  
 KEYWORDS capsid protein; L1 gene.  
 SOURCE Human papillomavirus.  
 REFERENCE 1 (bases 1 to 686)  
 AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur  
 Hausen,H. and de Villiers,E.M.  
 TITLE Specific types of human papillomavirus found in benign  
 proliferations and carcinomas of the skin in immunosuppressed  
 patients  
 JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
 MEDLINE 94340583  
 REFERENCE 2 (bases 1 to 686)  
 AUTHORS Shamanin,V.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
 Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld  
 242, 69120 Heidelberg, FRG  
 COMMENT HPVVS75 was isolated from a skin wart biopsy of a renal allograft  
 patient. It was found in a search for HPV DNA in 118 skin  
 lesions taken from 46 renal allograft patients [1]. HPV-24  
 appears to be the most closely related known type.  
 NCBI gi: 562318  
 BASE COUNT 208 a 122 c 164 g 192 t  
 ORIGIN  
   1 gggagaggac agccattagg cgttggtacc agtggacatc cactgttaa caaatgtt  
   L1 cds ->  
   61 gatgccgaaa atcccttagc ttacagggca caggcctttt ctactgatga taggcaaaac  
   121 acatccttg atcctaaaca aatacaaattt tttataatag gttgtgcacc ctgtattgg  
   181 gagcattggg atgttaggtga acgttgtgca ggagccaata atgaaaaatgg tcgatgcccc  
   241 cctattaaat tggtaaattc agtcatccaa gatggagata tggcagatat tggttatgga  
   301 aacctaaattt tccgtacctt acaggaaaaac agatctgatg taagttttaga tatagtgaat  
   361 gaaacctgtta aatatccaga cttttaaag atgcagaatg atatatatgg cgattcttgc  
   421 ttttccttg ctcgcccggga gcaatgttat gcaagacatt ttttgcggatgggggttaag  
   481 gcgggggatg acattccctgg tgccgaaatc gatgcaggta catataaaaa tgattttac  
   541 atacctggag cgtcaggta gacacaaaaag aatataggta actcgatgtt aatcccaaca  
   601 gtaagtggct cattgggttc tagtgatgtt caattgttta ataggccctt ctggctccaa  
   661 cgggcgcagg ggcaaaacaa cggaaat  
       L1 cds ->  
 //

**HPVVS92**

LOCUS HPVVS92L1 674 bp DNA VRL 15-NOV-1994  
DEFINITION Human Papillomavirus vs92-1 DNA, part of L1 ORF.  
ACCESSION X79949  
KEYWORDS capsid protein; L1 gene.  
SOURCE Human papillomavirus.  
REFERENCE 1 (bases 1 to 674)  
AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur Hausen,H. and de Villiers,E.M.  
TITLE Specific types of human papillomavirus found in benign proliferations and carcinomas of the skin in immunosuppressed patients  
JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
MEDLINE 94340583  
REFERENCE 2 (bases 1 to 674)  
AUTHORS Shamanin,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld 242, 69120 Heidelberg, FRG  
COMMENT HPVVS92 was isolated from a skin wart biopsy of a renal allograft patient. It was found in a search for HPV DNA in 118 skin lesions taken from 46 renal allograft patients [1]. HPV-9 appears to be the most closely related known type.  
The partial L1 sequences for HPVRTRX3 does not overlap with that of HPVVS92; from their similarity to HPV-9, it is possible that HPVVS73 and one of the other two isolates are from the same HPV type.  
NCBI gi: 562320  
BASE COUNT 223 a 110 c 141 g 200 t  
ORIGIN  
1 tcaaggggac agccattggg tgttaggaaca tcaggtcata ctttatttaa caaagtccagg  
L1 cds ->  
61 gatactgaaa actcaggtaa ctatcaagca gtttcagg atgacagaca aaatacatct  
121 ttgtatccta aacaagtgc aatgtttgtc attggctgt tgccgtgtat gggtaacat  
181 tgggacaaag ctaaggttt tgaatcagaa gcaaataatc aacaaggctt atgtccaccc  
241 atagagttaa aaaattcagt aattgaagat ggagatatgt ttgatataagg ctggaaat  
301 attaataaca aagcactatc ttataacaag tcagatgtt gttagatat agtaatgaa  
361 gtgtgaaat atccagactt tttaaccatg gctaattgt tgatggaga tgcttgaaaa  
421 ttctttgcta gacgagaaca atgttatgcc agacatttt ttgttaggg aggcaatgtt  
481 ggcgatgcaa tccctgatgg agcagtacaa caggatcaca actatttt acgtgcacaa  
541 aatgcacagc aacaacacac cttggaaat tctatatatt atccaactgt tagtgggtct  
601 ctgttaacat ctgatgctca gttatataat agaccattt ggttacaacg tgctcaagga  
661 caaaacaacg gtat  
L1 cds ->  
//

LOCUS HPVVS102L1 674 bp DNA VRL 15-NOV-1994  
 DEFINITION Human Papillomavirus vs102-4 DNA, part of L1 ORF.  
 ACCESSION X79946  
 KEYWORDS capsid protein; L1 gene.  
 SOURCE Human papillomavirus.  
 REFERENCE 1 (bases 1 to 674)  
 AUTHORS Shamanin,V., Glover,M., Rausch,C., Proby,C., Leigh,I.M., zur  
 Hausen,H. and de Villiers,E.M.  
 TITLE Specific types of human papillomavirus found in benign  
 proliferations and carcinomas of the skin in immunosuppressed  
 patients  
 JOURNAL Cancer Res. 54 (17), 4610-4613 (1994)  
 MEDLINE 94340583  
 REFERENCE 2 (bases 1 to 674)  
 AUTHORS Shamanin,V.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-1994) to the EMBL/GenBank/DDBJ databases. V.A.  
 Shamanin, Deutsches Krebsforschungszentrum, Im Neuenheimre Feld  
 242, 69120 Heidelberg, FRG  
 COMMENT HPVVS102 was isolated from a dysplastic wart biopsy of a renal  
 allograft patient. It was found in a search for HPV DNA in 118  
 skin lesions taken from 46 renal allograft patients [1]. HPV-15  
 appears to be the most closely related known type.  
 NCBI gi: 562310  
 BASE COUNT 223 a 102 c 148 g 201 t  
 ORIGIN  
   1 ggaagaggc tccatggg tgttagtaca gcaggccatc cactattcaa taaagttaga  
 L1 cds ->  
   61 gatacagaaa ataatagtgg ctatcaagat acgtctacgg atgacagaca aaatacatca  
 121 ttgtatccaa aacaagttca aatgtttgtta gttagatgtg ctcctgttt gggagaacat  
 181 tgggataaaag ctcctgtctg tgactcagat aaaaataacc aggctggaaa atgccttcca  
 241 tttagaactga gaaacacagt aatagaagat ggagatatga ttgatatagg ctggcaat  
 301 ataaaacaaca aggttttac agttactaag tcagatgtt gtctggatat agttaatgaa  
 361 acttgtaagt atccagattt tttaactatg gccaatgtat tatatgttgc ctcttgaaaa  
 421 ttctttgcaaa ggagagaaca gtgttatgct agacattatt atgttaggg aggtgttagta  
 481 ggtgatgcta ttccctgtatga agctgtgaat caagataaaa actttgtt acctgcacaa  
 541 ggcactcagc aacaaaagga tatacgatgt tctatataatt ttccaactgt tagtggttcc  
 601 ttagtaactt ctgatgctca attatthaac agaccatttt ggttacgcag agcacaaggg  
 661 caaaaataacg ggat  
   L1 cds ->  
 //

# Group B2 Sequences

**HPV4      HPV48**  
**HPV50     HPV60**  
**HPV65**

## INTRODUCTION

Group B2 is equivalent to part of the old group G. It consists of the human papillomaviruses HPV-4, HPV-48, HPV-50, HPV-60, and HPV-65, a group primarily associated with the benign cutaneous lesions, commonly seen in the general population. HPV-50 is the only member of this group associated with EV lesions. A number of apparent new types belonging to this group have recently been isolated [1], but no published information is currently available.

HPV-4, in conjunction with HPV-1 (group E1) and HPV-2, (group A4) are the major etiological agents of benign cutaneous papillomas in the general population. HPV-1 is primarily associated with deep palmo-planter warts, while HPV-4 has been correlated with common warts and keratotic flat lesions on the hands and feet [2,3]. HPV-4 is also frequently present in hand warts of meat handlers [4]. HPV-65 has been linked to pigmented common warts and keratotic flat lesions [3].

HPV-4 and HPV-65 produce homogeneous intracytoplasmic inclusion bodies in most infected epidermal cells. The inclusion bodies primarily contain E4 proteins that can be used to histologically identify these viruses.

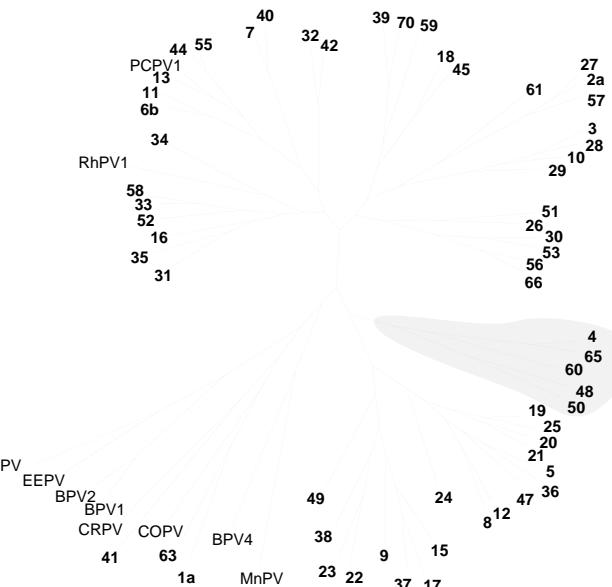
The primary target tissue of the Group B2 viruses is the epithelium, however rare mucosal infection has been reported for HPV-4, which has been identified in isolated cases of both normal and malignant oral lesions [5].

### What's new?

The complete genomes of HPV-48, HPV-50, and HPV-60 have been released since last year's publication and are given on the following pages. The sequences of other members of this group were published in *Human Papillomaviruses 1994* pp. I-G-8, and I-G-2.

## References

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- [4] Melchers,W., de Mare,S., Kuitert,E., Galama,J., Walboomers,J., van den Brule,A.J. Human papillomavirus and cutaneous warts in meat handlers. *J Clin Microbiol* **31**: 2547–9 (1993)
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**HPV48**

LOCUS HPV48 7100 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 48, complete genome.  
ACCESSION U31789  
KEYWORDS .  
SOURCE Human papillomavirus type 48.  
REFERENCE 1 (bases 1 to 7100)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Muller,M., Kelly,G., Fiedler,M. and Gissmann,L.  
TITLE Human papillomavirus type 48  
JOURNAL Journal of Virology 63 (11), 4907-4908 (1989)  
REFERENCE 3 (bases 1 to 7100)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV-48 DNA was isolated from a squamous cell carcinoma of the hand  
of an immunosuppressed 36-year old female patient; the DNA was  
present in episomal form. HPV 48 was not found in any of the 21  
similar tumors subsequently tested. Weak hybridization was observed  
under stringent conditions with HPV types both of the EV-associated  
groups and the anogenital-associated groups. HPV 48 is  
phylogenetically associated with HPV 4, 50, 60 and 65, a set of  
primarily cutaneous types.  
BASE COUNT 2286 a 1163 c 1447 g 2204 t  
ORIGIN 102 bp upstream from beginning of E6 cds  
1 tctgacgcataataattgtt ggcaacaatc gtgcataata acttaggaac cgagacagta  
61 tcaTATAAAT actgctgaac agtagatttc ttcaagaact gATGgagcca caatttccta  
E6 orf start -> E6 cds ->  
signal ->  
121 ctgatttggaa ttcataactgc aaatattttt acataagctt ttttactta gttcttaagt  
181 gatatcttttgc taaattttct gtatctattt ttgatcttgc ttctttcat aacaaacgcac  
241 tgtctgtaat ttggagagat aatacaccat ttgcattttt tactaaatgt ttaagattaa  
301 ctgcattata tgaaaaagat aatttttttgc tctgtactgc aaaaagtcat ttgttaactg  
361 gtttagttaa aaaggaatttgc tcagatattt atatttaggtt ccaacattgt tattcatttt  
421 tagatttattt agaaaaatttgc taccatttttataatgttgatgt tgattttctg tTAAttcgcg  
E7 orf start ->  
481 ggacttggag aggtgtttgtt agaaaatttgc tcagccATGa ggggagaTAA ggctactatt  
E7 cds -> <- E6 end  
541 cctgacatag agtttgcataa gcttggggc cctgcttaact taatttcttgc cgagtcttgc  
601 tcaccatgtt ctactgcataa ggaggagttt tgcgttgc tccatgttgc ggatagactc caagtgtcac  
661 aatttgcgtt gtcgcataa ggttgcacatgc gtcgcataa aatttggaaat acgttgggg  
721 gagcaactgt tacTGAAaga gcttggggc ttttgcgttgc cgtgcgttgc acaacttccc  
E1 orf start ->  
781 cgcaATGgca gatcaTAAag gtactgataa tatttgcataa aatgtatgtt tagatgggtc  
E1 cds -> <- E7 end  
841 ttgggttttataacttgcataa ctgaaatgttgc ggacgatacg ttatgtggatt ttgttgggg  
901 gagcacaat gactctgttgc ttttgcataa gtttgcataa ttttgcataa ttttgcataa  
961 gaatttgcataa gaaatgttgc gtttgcataa ggatgttgc aatgttgcataa atgttgcataa  
1021 tgggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
1081 agcatcttgcataa cggagactgtt ttttgcataa ttttgcataa ttttgcataa ttttgcataa  
1141 tactatttgcataa gtttgcataa ttttgcataa ttttgcataa ttttgcataa ttttgcataa  
1201 gtgtgaactt aatttgcataa ttttgcataa ttttgcataa ttttgcataa ttttgcataa  
1261 taaaatgttgcataa ttttgcataa ttttgcataa ttttgcataa ttttgcataa ttttgcataa

1321 atgtacACCA AATTGGGTaa taacagcaat aggtattaga gaagatttac gagatgcttg  
 E2 binding ->  
 1381 taaagttta ttacagcaac atgtttagtt ttagaaatg atttgcattt atttttctgt  
 1441 gctactattt gtagaatttta aggttactaa aaatagagaaa acggttttaa agttaatgt  
 1501 tagtatgtta aatgtctaaag aagaacaaat tttgtgtgaa ccgccaaaat tgaaaagtac  
 1561 agctgcagct ttatatttct ataagaagat tataactgtat acatgtttt aatatggcac  
 1621 ttgccttcc tgggttagta gattaactat agtagaacat cagtagctt cagcagacac  
 1681 atttcattt tctgaaatgg tacaatgggc ttatgacaat gatTTTACTG aagaagcatc  
 1741 tttgtcttat aattatgtat gttatgccac agaaaataca aatgcagcag ccttttttagc  
 1801 cagtaatatg caagtttgtt atgttaaaga ttgtgttaga atggtttagaa tgtagaaaaag  
 1861 acaagaaatg aaatcaatga caatgtcaga gtggatttcc aaatgttta aagaagaaac  
 1921 tattgtgaa gatgtggaaag aaattgtaca gttttaaaa tatcaggag taaactttt  
 1981 agaattttta atagctttaa aacaattttt taaatgcact cctaaaaaaa tgtagtata  
 2041 aatatatggt ccaccagata ctggaaaatgc aatgttttgc tttaaatttag tacaattttt  
 2101 gaaaggtaaa gttgtatctt atattaacaa atcgagttag tttgtttaa tgccattaca  
 2161 agatgtctaaat ttgggtttgt tagatgtgc cacacataat tgtagtattt atttagacac  
 2221 atatttgaga aatgcattt atgttacac gttttgttta gatattaaac ataaaaacact  
 2281 gcaacagaca aaacttccac ctatgataat aactactaat gttaatgtaa caactgtatg  
 2341 atctctattt tatttgagaa gttagacttac gtgtttcaat ttccgaaata agttaccaat  
 2401 gtctgacaaa gatgaacctt tgtttaccat ttctgacaaa agctggacct gtttttttag  
 2461 aaagtttgg aatcaatTAG aactcaaga agATGcagcc agagacccag gagagcctga  
 E2 orf start -> E2 cds ->  
 2521 gcacccgttt tgctgcacag caagaatttgc agttgacttt gatTGAaaaaa gaatctttag  
 <- E1 end  
 2581 atcttaaaga tcatttagca tactggaaag ctgtttagatt agaaaatgtt attcgcattt  
 2641 atgcttagaaa agaacatatt actaaatttgc ttgtcgaccc attaccaaca tttagctgt  
 2701 ctgaatataa agcaaaagaa gcaattata tacagctgt tattcaaagt ttattgaaat  
 2761 cagagtttgc ttggaaaga tggactctt cagaaacttag tgcaaaaaact ataaacagtt  
 2821 cccccagaaaa ttgtttcaaa aaagtacccctt tcattgtaaa tttatgtttt gataatgt  
 2881 aaagaaattt ttttcctt acctgttggg attttatata ttatcaagat gacccaaaca  
 2941 aatggcacaat gactgaaggg ctgttgcata ataatggatg ttattatgtt gatctaaatg  
 3001 gtgatTTTGT atacttact ttatttcaac ctgtatgtt AAaatatggaa aaaactggac  
 E4 orf start ->  
 NH<sub>2</sub> terminus unknown  
 3061 tatggacagt tagatttaaa aacaaaacta ttctgcctc tgttactgc tcctcgagaa  
 3121 atacaatcc ctcttctgaa agcagggtcg ggctctgcac ctccagcagc tcggagagcc  
 3181 ctcgaaggag accgagcatc tcagaaaact ccaacaccga gtcgcccacc tcctcgacat  
 3241 ccagactacg agagcgacga cgacgagaac cgagagaatc tggaccaccac  
 3301 ccagaagacg aggaacaaag agggaaatttgg ggtccgactc tgccaccaact cttcgaaag  
 3361 tggatcaag atctacaacg ctgttgcac acgttactc acgacttggc cgattacagg  
 3421 aagaagctcg ggatccgcca tTAGtggat ttacaggtca acaaaataat ttgaaatgtt  
 <- E4 end  
 3481 ggagaaatcg ctgttactaca aaatatgtt gttttttttt atgcttcagc tctgtttgg  
 3541 atggcttgg tcctaatttctt gatgggggtt ctgcaaaaatgtt gttttttttt ttttttttt  
 3601 atgcccacaaat acaagtgttca ttaaacacat ttcatattcc taaaggaaact actataact  
 3661 tggaaagact TGAcgttta TAATGtcctt acgttagaaga aaaagagcaa gtcctactga  
 L2 orf start -> <- E2 end  
 L2 cds ->  
 3721 tctttataaa acatgttgc aagggggggaa ctgcatttcc gatgtaaaa ataaatttga  
 3781 aaattctact attgcagatt ggttATTAAA aatatttggaa agtttggat attttggaaa  
 signal ->  
 3841 ttggaaata ggatctggaa aagggtctgg gggatcattt ggatatac cattaggatc  
 3901 cgcaggaaatg ggaagaccat ccacagactt accagtactt agacctaattt ttgtgtat  
 3961 acctataggt cctcaaagta tagtacccat tgatcctgaa gcgtcatcta tagtccctct  
 4021 tttgttggaa gggcctgata tatctttat tgcaccat gcaaggccat gtataggagg  
 4081 tgaggatattt gaaacttca ctttagaga tccagcaact gatgttaggtt gtgttagtgg  
 4141 aggtcctactt actatttctt cagaagaaag tgagacatg ataatagatg ctttaccaag  
 4201 tgccacaact cccaaacatg tttttatgtt ttcttataca caaactatct tgcaaaacaca  
 4261 gttttttttttaata atgttattttt tgataactat gttttttttttag atccattttt

## HPV48

4321 tgcaggagag acaattgggg acaacatatt tgaagagata cccttcaga atttaaattt  
4381 cagtttccg cggaaagta cacatgtta acctggagg ggtttaccaa caccagctca  
4441 aagatcttac agtagattt tggAACAGTA cccatccaa gctccggaa ttcttagtca  
4501 gccttcgtcgat ttgggtcagt ttgagttga aaatcccccc tttgatccag atatttagat  
4561 acagttcccg cgtgatgtaa atagcctaga ggctgcgcca aatccagctt ttgctgacat  
4621 tgcttattta agtaggcgc acatgtctgc tacatcagaa ggatttagtca gagtcagcag  
4681 aattggatct cgagcgttat tacaaaccag gagtgattactataggcc ctaaaagtaca  
4741 ttattatatg gatttgcgtcaatatcaac agaagctata gaattgcaaa ccttgcaga  
4801 ttctggacat gttcacacaa tagtgcgttca ttcttataca gttactgctt tagatgatcc  
4861 agcaaatata gctgatataa attatacaga agatgattt ttagatcctt tacttgaaaa  
4921 cttaataat tcacatatta cagtacaagg gggttgcgttag gaaggagaaa cagttgctct  
4981 tccaattcct tcaattacta attcttccaa aactttgtt acagacattt cagaaaatgg  
5041 tctgtttgc aatgatacag atagtctttt aaccccagca agcactattt tacctgctat  
5101 taattgggtc cctttatgg atagttactc agactttgtt ttagatcctt ttttattcc  
5161 acgtaagaaa cgacgctTAG atatccttTA Atgttttca gATGgctctg tggctgcag  
L1 orf start -> <- L2 end  
L1 cds ->  
5221 tccctggcaa ggtttaccta cctccttagtgc accaggtagc tcgtgtgttgcgcactgatg  
5281 aatacgtgca agaaacggat gtatattttt atacaagcac taaaagactt ttaatagtt  
5341 gtaatccta ttttgcgtt gaaaacagag acactataac agtacctaaa gttctgcta  
5401 atcaataccg agtatttgcgtt tgtaaacttc cagatcctaa caagttgtctatgttgcata  
5461 aaaatttata taattcagat aaggaacgtt tagttggaa acttgcgttgcgttgcata  
5521 gcagaggggg tcctcttgcgtt gtaggtctca caggtcatcc ttactaaat aagataggg  
5581 acacagaaaa tccttagctt tatttaggaa aacaaacaaa ggatgagaga caaaatgtt  
5641 ccatggatcc taaggcgtt cagatactaa tagttggttt tgctccagcc actggagaat  
5701 actgggattt agctaaacca tgcaatgattt tggaaaacgg ggctgcacca ccaattcaac  
5761 tagttaatac tggttattcgtt gatgggtata tgggagatag aggcttggg gctgctaatt  
5821 ttccctaagtt gatgcaggat cgtgctggcg tccctctaga gttaatagat tctattagta  
5881 tatggccaga tttttaaat atgaccaaaat atattttatgg agactctgtc ttcttttttgc  
5941 gtaaacggga acaatgttat gctcgatc ttttgcgtt gactggccaa atggggggagc  
6001 ctataccaac agaaaatggaa gtatattata taactctgtt ttctggccgtt caaaacaaca  
6061 gatcttctca tttaggatct tctgtgttattt tacaacacc aagtggatcc ttgaaatacta  
6121 gcgattctca gttatataat aggccattt ggcttagacg agcccaggaa acaaataatg  
6181 gcatttgcgtt gggaaatggat cgttttgcgtt taataactcat aatgtgaatt  
6241 ttactattatg tggttgcgtt gataaaacttgcgtt cattaaacttgcgtt aaactacata gataatgtt  
6301 acaaataataa taatgcgtt gtttacaaat atcttcgtaca tacagaagaa tatgaaatag  
6361 agttggttt tcagttatgc aaagtgttactc tgactgcgtt tggttgcgtt catttacacg  
6421 ttatgaatcc cagaatatttta gaggagggttgcgtt aatgttgcgtt gctccaaacgg  
6481 gcattgaaga tacttacagg tataatccat ccatggctac taaatggccct actgctgtt  
6541 cagaagaaga cacagatcca tacaaacgtt acagtttgcgtt gacttttagat atgacagagc  
6601 gcttctcgatc tgatttaatg cagtttgcgtt tggttgcgtt atttttat caaactgtt  
6661 tggttgcgtt gaaacgttactc agaagacttgcgtt aggatctgtt accagatctt  
6721 caaagcgttag gagatgttgcgtt TAGttaatggat gtagatgtt tacatttata atactgtt  
<- L1 end  
6781 tcaaacaacat tgcgtatcAAT AAAActgttgcgtt aatatttttgcgtt cttatcgcc  
signal ->  
6841 tccattgggtt ggggttgcgtt cttatcgatc ctgggtcagt ctttgcgtt cttatcgcc  
6901 aggaggcgttgcgtt gacgatttcgtt acgttccattt gtgagacgaa gACCGTTTTC GGTaaatgtt  
E2 binding ->  
6961 atagccgcca ggtattgtttt gtaccgttgcgtt agtttacccat taaaatgttac tgccaaacttt  
7021 tacaagttca gacagatc aacaagatcat cttttttttttt cttttttttttt  
E2 binding -> E2 binding ->  
7081 CGTTTGTGGT atgttgcgtt  
//

LOCUS HPV50 7184 bp DNA VRL 17-JUL-1999  
 DEFINITION Human papillomavirus type 50, complete genome.  
 ACCESSION U31790  
 KEYWORDS .  
 SOURCE Human papillomavirus type 50.  
 REFERENCE 1 (bases 1 to 7184)  
 AUTHORS Delius,H.  
 JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
           Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
           I.N.F. 506, W-6900 Heidelberg, Germany  
 REFERENCE 2 (sites)  
 AUTHORS Favre,M., Obalek,S., Jablonska,S. and Orth,G.  
 TITLE Human papillomavirus (HPV) type 50, a type associated with  
       epidermodysplasia verruciformis (EV) and only weakly related to  
       other EV-specific HPVs  
 JOURNAL Journal of Virology 63 (11), 4910 (1989)  
 REFERENCE 3 (bases 1 to 7184)  
 AUTHORS Farmer,A.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
       Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
       NM 87501, USA  
 COMMENT HPV50 DNA was isolated from actinic keratosis taken from a  
       epidermodysplasia verruciformis (EV) patient, who had previously  
       been found to be infected with HPVs 5, 8, 20, 23, and 36. HPV50 was  
       not found in cutaneous lesions of patients with warts (56 cases),  
       keratoacanthoma (12 cases), Bowen's disease (20 cases), actinic  
       keratosis (25 cases), basalioma (24 cases), and squamous cell  
       carcinoma (22 cases). It was however found in specimens of skin  
       macules of 2 out of 34 additional patients suffering from EV.  
       Phylogenetically, HPV50 is a member of a group of primarily  
       cutaneous types including HPVs 4, 48, 60 and 65. HPV-4 and HPV-65  
       are associated with Hg-ICB. The members of this group other than  
       HPV-50 are not specifically associated with EV.  
 BASE COUNT 2333 a 1205 c 1441 g 2205 t  
 ORIGIN 102 bp upstream from beginning of E6 cds  

```

    1 tctatcta ataatgttgc aacaattttt agacatagag acgtgacaAC CGACTACGGT
          E2 binding ->
    61 gcaTATAAAA gagctgatca gcacagattT GAaggagact gATGggcct cagagagcta
      signal ->           E6 orf start -> E6 cds ->
    121 aaaattttgtt ggacttgc aagcaacaac agataggattt ttttgaatta gagctacagt
    181 gcttgggggg taaattttgtt attactttgc ctgacttagc tagcttcat tgaaaaaagt
    241 tagctttgt ttatagagat ggttattgc ttgctgcgtg cgcttaatgc ttaagattgt
    301 ctgctatctt tgaaaatgg agatattata ctgctctat aaaagcttac ttgcttatctg
    361 atttgattgg tagaccttg agtggaaatcg caattcgctg tgaaaattgt atgttttgt
    421 tggattatat tgaaaatgtac gattgtatggt gtacacgggg ttatttcat tTAGtttagag
          E7 orf start ->
    481 gtaattggag gggctgttgtt agaaaattgtt acgaacATGa ggggTGAtaa accaactatt
          E7 cds ->           <- E6 end
    541 cctgatattt ttttagaaga gcttgggggg cctgtgaatt tgcttagtga cgaatctatt
    601 gaaactgtatg acaTAGcaga atctgaaagg tcaccattca agattgattc tacgtgtaa
      E1 orf start ->
    661 cattgtcatt gtcgcgttag actgtgttgtt gtcgccaccc acgcagctat ccgtgtgttt
    721 gagtgccttc ttcaatcaga atttttttt ctgtgtctta agtgcgtccaa agaatttgcta
    781 cggaaATGgca gaactTAAG gtacagataa taattcta at gtagaaatta ttaatgagtt
      E1 cds ->           <- E7 end
    841 gtttgcataat gaagctgtct gtatgtatgtt ttcttttcag gaatttttg atgaaagtac
    901 ggtatgtatctt actatctcta atttatata tgactctgaa aacgtgtgc agggaaattc
    961 ccatgcattt ctaaatgcac agcttcaga ggaatatgac aaagacctgg ttacagtaaa
    1021 acgaaagttt tatgccaccc cggaaaagct cgcctctgtt ttgatccga gactttcagc
    1081 ggtgcataata acaccagaaa gacaatccaa aaggcgttta ttagagaca gtgggattga
  
```

## HPV50

1141 agatgaagct gaaaattcta ttgttcagg acaggatgat agttcaaatg tggcgggaaa  
1201 caaaaatggc gctgatgcgg agttgttattc gttgttcat agcaataatc gttagagctgc  
1261 ttgccttgt aagtttaaag aaaaatatgg cattccatt aatgaaatta ctagaacttt  
1321 taaaagtaat aagagtgt aacaaaattt gattattgtt gttttgcct gtgcagaaga  
1381 ttaattgaa gcttctaaaa ccacgatgca aaatcatgtt tcctatttac aaatgattac  
1441 ttctgatattt tcagcttgc atattatttgc cttaaaggct gctaaagagca gagagactgt  
1501 tgtaaattt attaataatgc tgctaaatac aaaagaggaa caagtaactat gtgatcctcc  
1561 taaaataaaa agtatggctg cagcattata ttgctataaa aaggtaatag cagatacctg  
1621 ttataaataat ggagactttc ctgactggat agccacacat actgttataa atcatcagct  
1681 agcaactgca gacagctta aatttagtga tatggtacag tggcatacag ataatgatat  
1741 gctggatgaa gctgcaatttgc cttacaattt tgctgtctat gcaagtggaa atgaaaatgc  
1801 agtcgcattt ttacaaacta atgtcaatt aaagtatgtt aaggaatgtt gtgcaatgg  
1861 caggttatac aaaaagcaag aaatgaggaa tatgactatg ccagaatgga taaaatcatg  
1921 tttcacaaat aattataatt ctgatgattt gaaagttatt gtaagatatt taaaatcatca  
1981 aaatattaac tttttagaaat tttttagtgc tttaaaagttt ctttaaaag gcatacctaa  
2041 aaaaatgtgc ttagttattt atggaccacc agatacaggc aagtcaactt ttgttatca  
2101 atttattcag tttatgagag gaaaagttgtt atccttcattt aacaaaataa gtcatttttgc  
2161 gtaatgcct ttatttagatt caaaaatagg attttagat gatcaactc aatgttgg  
2221 gatgtatttgc gacacacaca tgagaaatgc atttgtatggt aatgcagttt ctgttgatgt  
2281 gaaacataaaa aatttacaaac aaatagttt accacctatg ttaataacaa caaattgtga  
2341 tgtagcaga gatccaacgt ttatgtactt aaggagtaga ttaacatgtt ttaactttcc  
2401 aaataagttt ccattgtatg aaaatggaga accaaaattt aaatttactg ataattgctg  
2461 gacgtctttt ttttagcaagt ttttggaaagca ctTAGatttta cctgaagATG acccagatgg  
                                E2 orf start -> E2 cds ->  
2521 agacacagga aactctgagc gcacgttttc ttgcacaaca agacattcaa ttgaatctga  
2581 tTGAaaaaga ttcaaaaaat tttaaaagacc atatacgacta ttggaaatct atgagaaaag  
                                <- E1 end  
2641 aacaagtgc tgcattttat gcaaaaaaaag aaaaatatgag caggcttggaa ttacaacctc  
2701 tccctccctgc taaggtttgc gagaaaaaaag caaaagatgc aatttgcattt caattacttt  
2761 tgcaatccctt gtataagtct gattttgggt ctgaaccatg gactttatca gaatgtatgtt  
2821 tagaaatgtt aaatgcacct cctagaaattt gttttaaaaa acaaccgtttt actgttaactg  
2881 tgcaatttgc caatgtatcc taaaatgtgtt atccttatat atgttatgaa tatatatatt  
2941 atcaagatga tagagacaaa tggcataaaag tttaagggtt atgttgcac aatggccctt  
3001 attttaaaaag aTGAActgtt gattcagttt atttttaactt ctttcaacctt gatgccactg  
                                E4 orf start ->  
                                NH<sub>2</sub> terminus unknown  
3061 tatatggcaa atctggacaa tggactgtt aattttaaaaa caaaaactatt catttcctctg  
3121 tcatacgctc ctcaaggaaatggc ctgtgtacgc acagccccggg ctttccacat  
3181 cgtacgacaa gagccaaacag gaaagatctg gaagcggtca accaaaagcc ctacaggaca  
3241 cccaaaccacc cacccgcaca tcaacagttt gacttcgacg aggacgacga gaaagagaaac  
3301 accatttcata cagacacaga aagtccat cagaatgggg agccgactct gcgcacactc  
3361 ctgaagaatgtt gggaaagaaga ttcacacag ttgcagcgc tggctgtca agacttagac  
3421 gattacaaga ggaagctcggtt gatccacccat tccTAAttat tacaggtcaa cagaataatc  
                                <- E4 end  
3481 tttaaatgtt gaggatataagg ttctcacaaa aatatgcaga tctctatgtatggatgt  
3541 ctgcatggaa gtgggtgggc cccaaatccatc agggatatacg gggtgtatgtt aatttgcattt  
3601 ttgcattttaa aatccTGAa caaaggctat cttttttaaa cactgttggaa ttacccaaaaa  
                                L2 orf start ->  
3661 atactacgtt ctctatggaa catttggact ctctTAATG ctgcagac gcaaacgggc  
                                <- E2 end  
                                L2 cds ->  
3721 aagccctacg gactttatata gatcatgtttt acaagggggg gattgcatac ctgatgttca  
3781 aATAAAAtttt gaaggcaaca caatcgacaa ttgggttatttggaaaatatttgg gaggtttatgt  
signal ->  
3841 atactttggc aatttggaa ttggaaacagg aagaggttactt ggggttactt ttggctatag  
3901 accttttggc gcccctgggt ctggaaaggcc aactcaggaa ctacccatcg caagaccaaa  
3961 ttgtgttata gatccatgtt ggccagcgcc tattgtacca gtagatccct ctgcagcttc  
4021 aatagtttca tttagtgcac ggcggccctgtt ttgtgttattt gcaatgttttttgc  
4081 tgcagcaggtt ggaactgtata ttgttattata tactataaca aattccacaa cagatgttgg  
4141 tgctgttgggtt ggtggggccca ctgttacctt taacgaagaa ttgttgcacatgtttaga  
4201 tgccacaacca attgcacccat atccaaagca atttattat gactctacta tagcagcaac

4261 ttttgaaca cagattaatc ctttcataaa tccagacata aataatgtta atgtattagt  
 4321 tgaccccagc ttgcaggag acactgttagg tgactacttt tatgaagaga tacctttgga  
 4381 acgtttagat attcaaacct ttgacatttt agagccacct actgaaagca cccccACCCA  
                                                                                         E2 binding ->  
 4441 ATTAGGTaat aggtttgtt ctagggcaag agatctgtac agtcgattt ttgcacagca  
 4501 gccaatatct gagccagatt tttttagtca accttcccgcc ttgttcagt ttgaatata  
 4561 aaatcccgcc ttgaccagg atgtgagcct atacttttag gggatttgg aaggcctcag  
 4621 ggcagcgcctt ttgcaggaat ttgcgtatgt agtttattttt ggcaggccaa gagtatccag  
 4681 cACCTCAGAA GGTacaataa gagtaagtag attaggtacc agagcagctt taacaacacg  
**E2 binding ->**  
 4741 tagtggtctt tctgtggac ctcaggtaca cttttatatg gatthaagtg atatacctcc  
 4801 agaggattct atagagtgc atacattaaa cgttacacca caaacaagta caattgtaga  
 4861 tgatatatta gcaacaacta catttgcata tcctgcaaaac tccttattta cacagttaa  
 4921 tgaagatgtt ttaacagacg atgtgacaataat ttttaca gatgttcatt tagttatacc  
 4981 agctactgtat gaagaaaatg acacagcaat aaatattttt aatthaagaa atattcctct  
 5041 tactgtggc atgaatttcg gtgacatatac tactacatta tcagattata atatttttaga  
 5101 tgcatttcctt atagtaaaat caaatgtttc tgaacagccc cttttgtt tagattttc  
 5161 agattatgtat ttacatccag gtcttctcc aaaaagaaga cgcatagatt attttTAAtt  
                                                                                         <- L2 end  
**L1 orf start ->**  
 5221 tattttacag ATGgctcatt ggtcctcaac ctctggaaag ttataccttc caccaggatc  
     L1 cds ->  
 5281 tcctgttgcc agagtttaa gcaccgatga atatgtgaaa gaaactgtat tttactttca  
 5341 tgcacgcagt gaggcgttac taattgtggg acacccatat tatgtatata gaggatgggg  
 5401 agatatcaa gttcctaaag ttcacggaaa tcaatacaga gttttcggtt gtgaattacc  
 5461 agatcctaacc aagtttgcata taattgtatc tacattgtat aactcagata cagaacgtt  
 5521 ggtttggaaa ctagtaggtt tagaagtccgg gagaggtggg ctttaggtt ttggatctac  
 5581 tggcatccc ttgtttaata aggttggaga cacagaaaat ctttagttt acttaggtcc  
 5641 acaagaaaaaa gatgaaagac aaaactgtc tatagatctt aaacaaacac agttattgtat  
 5701 ttaggctgc aaaccgcgtt ttggtaata ttgggattt gcagaacctt gtgacaaaaaa  
 5761 cagcttaat aatggcaagt gtcctccaaat acaacttagta aacagtttata ttccaggatgg  
 5821 tgatatgggaa gatataaggat ttggtaatgc aaactttctt aaactacaac aggacagagc  
 5881 aggggtccctt ttagatatac tggattcaat cagttatgg ctttagtctttaaaaatgac  
 5941 taaagatgtc tatggggacc atgtgtttt ctatgcaaaag caagagcaat tatatgccag  
 6001 acattttttt acccatgcag gaccaattgg ggaacctata cctaattgtct caggatttt  
 6061 taattatgca gtaaacccta atcaaccaga gcaaaatcgt agaACCAATA TTGGTtccta  
                                                                                         E2 binding ->  
 6121 ctatattttt actacaccaa gtggatctttt aatacaagc agttcacagt tatttaatag  
 6181 accatattgg attcgcagag ctcagggtac gaacaattgtt atttgggg gtaatgaggt  
 6241 atttggatca gtttttgcata acacccggaaa cttttttttt aatatttagt gtttttttt  
 6301 tgtcaatcctt ttggatcctt taaatgtac aagttttttt atgtactcaa aggttatttt  
 6361 taatcgtac agccgtcata ctggaaataa tttttttttt agttatgttttttttttttttt  
 6421 agtaggattt gatgtgtata ttttttttttttttttttttttttttttttttttttttttttt  
 6481 aaattggcaa ttatgttttttttttttttttttttttttttttttttttttttttttttttttttt  
 6541 cttaaaatctt gatgttttttttttttttttttttttttttttttttttttttttttttttttt  
 6601 ttataaagaa ttttttttttttttttttttttttttttttttttttttttttttttttttttttt  
 6661 tcgttatgcc cttaggacaa aattttttttttttttttttttttttttttttttttttttttt  
 6721 aactgatttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt  
                                                                                         <- L1 end  
 6781 tgctgacatg ctttcttggc ttttactgttata ttttttttttttttttttttttttttttt  
 6841 gcttttagatc tgagtcttgc acatttcaca aaatgAATAA AcaAATAAAa ttaatgtaca  
                                                                                                 signal ->signal ->  
 6901 ggtgtgtgtt gtcttttttttttttttttttttttttttttttttttttttttttttttttttt  
 6961 gcaacctctgtt gatcaatcat gttgttttttttttttttttttttttttttttttttttt  
 7021 gagacacgcAC CGTTTCGGT aatgttttttttttttttttttttttttttttttttttttt  
                                                                                                 E2 binding ->  
 7081 ggtacttgctt aacaaagata aaatcttcacg agtttttttttttttttttttttttttttt  
 7141 gcaatgttttttttttttttttttttttttttttttttttttttttttttttttttttttttt  
                                                                                                 E2 binding ->  
 //

**HPV60**

LOCUS HPV60 7313 bp DNA VRL 18-JUL-1995  
DEFINITION Human papillomavirus type 60, complete genome.  
ACCESSION U31792  
KEYWORDS .  
SOURCE Human papillomavirus type 60.  
REFERENCE 1 (bases 1 to 7313)  
AUTHORS Delius,H.  
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches  
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,  
I.N.F. 506, W-6900 Heidelberg, Germany  
REFERENCE 2 (sites)  
AUTHORS Matsukura,T., Iwasaki,T. and Kawashima,M.  
TITLE Molecular cloning of a novel human papillomavirus (type 60) from a  
plantar cyst with characteristic pathological changes  
JOURNAL Virology 190 (1), 561-564 (1992)  
MEDLINE 92410648  
REFERENCE 3 (bases 1 to 7313)  
AUTHORS Farmer,A.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,  
Los Alamos National Labroatory, T-10, Mail Stop K710, Los Alamos,  
NM 87501, USA  
COMMENT HPV60 was originally isolated from a keratinous plantar cyst  
composed of the wall of the squamous cell layer and the horny inner  
substance in the lower dermis displaying cytoplasmic amorphous  
eosinophilic inclusions and vacuolated structure with or without  
pyknotic nuclei. These morphological changes are not characteristic  
of skin lesions associated with other HPV types (1, 2, 3, 4, and  
7). HPV 60 was found in three out of three other plantar cysts  
with similar pathological changes; a fourth cyst without the  
associated pathological changes as negative for HPV60. These  
results strongly suggest that HPV 60 has unique biological  
properties which can induce a plantar cyst. The HPV60 genome  
appeared to be in an episomal form. HPV 60 showed no similarity with  
other known prototypes (HPVs 1-59) by Southern blot analysis under  
stringent conditions. Phylogenetically, it is associated with HPV  
4, 48, 50, and 65, a group of primarily cutaneous types.  
BASE COUNT 2431 a 1241 c 1462 g 2179 t  
ORIGIN 102 bp upstream from beginning of E6 cds  
1 tataggat acactgattt ttggcaacta tcattaaatc ataaaaaaaaa tatgACCAGA  
E2 binding ->  
61 AGAGGTATAT ATAAAtagct gagacgttcg taaaacttttag gATGcagatg gaagaagaca  
E6 orf start -> E6 cds ->  
signal ->  
121 ggtttccaac aacagtggct gattattgct ctgaatttga tattcctta aaagatctta  
181 agttaaaatg tgtatTTTgt agatTTTact taactgaaca gcagTTggct gcattttata  
241 ttaagaattt aaagtttagt tgaaaaacc gttattgct tgcttggct actccgtgtc  
301 tttagacttac tgctaaatTTttaa gaagctggaa actatTTtca gtgtatgtgt aaaggagaag  
361 tattagaagt tctaactcgT attccttga gttctttc tgtagcgtgt tttgattgcc  
421 ttacattgtt atcttttgcA gaaaaaatag attgtataat tagtggtcaa aacttttatac  
481 ttgtaagggg tcgctggaga tcatattgtt gaaatttgcA TGAgaaATGA ttggtaatca  
E7 orf start -> <- E6 end  
E7 cds ->  
541 gcctaattgtt aataacccttg atgtaaattt ggaggaggTTTg gtttacctg tcagtctttt  
601 agctgatgag gagttgtcac ccgatggta tcctggagg gaggagcact atccctatac  
661 aatagacacc tgTTgcaaac cttgtggagc aggtgttaga tttactatta ttgctactcc  
721 ttctgctgtt ataactttc gtcaactatt gttcaagaa gtgttctga cctgttTGAg  
El orf start ->  
781 gtgctccaga tcccttttc gacATGgcag atccTAAtaa aggtattaaat tctcttgaat  
E1 cds -> <- E7 end  
841 taaatgaggg gcatagcgaa tggatgttgc tgacagaagc tgagtgtatt aatagttgg  
901 atacaatggA agagctattt gaagaaagta cagatggatc tattgtgtcc aatctgtatag  
961 acgattccga ggaactggag gagggaaatt ccctggact ctacaatgaa cagttAACAG  
1021 agattgcaA tagagctatt ttagcgctaa aacgaaaggta aactaaaaca cctttgaaaa  
1081 gccaggacag aacgggttgcT gacctaagtc caaggttggA agctgtcaca atttcacctc

1141 agagacaaag caaaaggaga ttatttgagg acagtggatt aggagaagat gaagctacaa  
 1201 attctattga aaaaaaggtt gtttcaact ctttagagag taatgaaagt gggaccttgg  
 1261 ttgtggaaac ggacagtata tttcgagta ctaatagaaa agccactta ttggctaaat  
 1321 ttaaagaata ctttgggtt gcatatggag attaacgcg accgttaaa agtgatagat  
 1381 catgttgta aaactgggtt ataagtgtgt gtgccgtgc agaagaagta atagaagctt  
 1441 caaaaacagt tatgcagca cattgtgatt tttcacagg tatttcataat gggtttatg  
 1501 ct当地tattt ggtttttttt aaaacagcaa aaagttaga tactataatg aaatttattt  
 1561 ctttaacattt gaatgtaca gaacaacaat taatgtgtga tccacaaaaa tcttagaagta  
 1621 ccccaacagc tctttatgtt tagaaggt catttggaaa tgcatcgat atttatggac  
 1681 cgttccaga ttggtagca aaattaacta ttgttagacca tgaatccgccc gcgagctcag  
 1741 aacagtttga acttgctcaa atgattcaat ttgctttaga caataacttgc acaactgaat  
 1801 ctgaaatagc ttataaatat gcattgttag ctgatctga tgctaattgc gctgcatttt  
 1861 taaaaagtaa tcaacaggtt aaatatgtac gagactgtca tgcaatgtt agatattata  
 1921 aaagacaaga aatgaaagat atgtcaattt ctgagtgat atggaaatgt tgcatgattt  
 1981 gtaatcaaga gggcaactgg aaattaatag cacaattttt acgttatcaa gaagtttattt  
 2041 tcatttcattt ttatgtgca ttaaagacat tggtttaaagg tattccaaaa agaaattgtt  
 2101 tagtggggg gggacctcca gatacaggaa agtcttataat ttgttctca ctacacgg  
 2161 ttatgcaggg aaaagtggta tctttcatga atagacacag tcaattttgg ctacaacctt  
 2221 tacaagattt taagcttggta ttcttagatg atgctacatt tcaatgttgg caatacatgg  
 2281 atgtaaatat gcgaaatgca ttagatggta atcatatttcc attagatttta aacataaag  
 2341 ctcccttaca aataaaatata cctcccttata taataactac caatgttggat gttggaaatgt  
 2401 aagcttagctt aatgttata aagtagtagac tagtattttttaa tgcatcatgg aacaatttac  
 2461 cttaaaaaga aaatgtatgaa gtactttatg aaattactgaa tgcatcatgg aatgtttttt  
 2521 ttatcaaattt tgcaagccat ttagagcTGA cagccagagg agacgagcag cATGaatcag  
 E2 orf start -> E2 cds ->  
 2581 gccgatctga ccgagcgttc cgatgcactg caggaacaaa tactgaatct atATGAgcaaa  
 <- E1 end  
 2641 gattcaagg acattcaggc ccaaatacaa tatttggatt taaatagaaa actatatgtc  
 2701 acatactattt atgcaagaaa agaaggctat tcgcatttgg gtcttcaacc cttaccagct  
 2761 ttgcaagttt cagagtacaa agccaagcag gcaatcgaaa tgggatttgg attaaccagt  
 2821 ttaagcaaat cccaaatatgc ttcaagacta tggggttttaa cagatacaag tgcaatgg  
 2881 ttatcaaccctt ctcagaaat tacattttaa aagaaggat atactgTAAa tttttttttt  
 E4 orf start ->  
 NH<sub>2</sub> terminus unknown  
 2941 gataataatg aaaataatac atttccctat acaaatttggg aatataatttta ctatcaggat  
 3001 gatattgaac aatggcacag gaccagagga gagggtggact ataatttttttca  
 3061 gaaaataatg gaaatagagc atattttctc ctatttgata gtgtatgcaca aacatattca  
 3121 caaaactggaa catggacagt gcattttaa aaccaatttttta ttctgtcttcc ttttaccagg  
 3181 tcctcaaaac aatccctccga cgactacact tccaaagccg ggcagcaacc ccactcttcc  
 3241 gcctcatctt catggccgac tactaccggc ggaggacaga cctcacaaga gggagtctct  
 3301 agctctacca cgtcgccgag tgctgttgcgatgcacccgaa gaagatccaa cgagcaacaa  
 3361 agagaactat cctccagaga gtcgccccgtt accaaaaagac gcagagtacc cgacgaagtc  
 3421 gaccgacaga gtcgccccgtt accaaaaagac gcagagtacc cgacgaagtc  
 3481 tctcttccta gaagcgttat atcaagactt gcaagactt aaggagaagc tcggatcct  
 3541 ccaatccctgc TAAattaaagg tctagcaaac tcccttaat gttggagata tcgattgaaa  
 <- E4 end  
 3601 aagtatacac gttattttaa atgtatgtt acagtattttt gatgggtttaga catagacgtt  
 3661 ccagaatctt ctagacataa attgttagtt gtttttaATG Ataccacaca acgagatgtt  
 L2 orf start ->  
 3721 ttatgaaat tagtaactttt gccaagaggt tgtagatata catttggaaat attaaactct  
 3781 ttgTAAtatt tgtaaaacaa aacaaaATGt atgcttagatg aaagcgttggaaaagagact  
 <- E2 end L2 cds ->  
 3841 ctgtgaaaaa cttatataaa caatgtcaac ttgtgtgtca ctgcctctt gatgtacgaA  
 signal ->  
 3901 ATAAAgtaga aggaaccaca cttgcagatc gattttaca aatatttgg agtatctt  
 3961 acctggggaa ttgggtata gggacaggta aaggatcggtt ggggtgtaca ggctataac  
 4021 ctcttggatc tgcaagatgtt ccagggtcta cacctggaaat agttataaaa cccacacgAC  
 E2 binding ->  
 4081 CGTTTCGGT tcctttatgtt ccaataggat ttggaaattcc atgcacaccc gtagggatgt  
 4141 gtttacctgtt ggacattata gatgccagtg cttccctat tatacccttgc caggaggtcc  
 4201 tgccagagac caccattata tgtagccgtt acagcggtcc tggattgggtt gcaagtggaaa  
 4261 ttgatataatgtt ttcagaacca agACCAGATG TGTTcggtgt tgataactca ccaacagtt  
 E2 binding ->  
 4321 atacctccat tgataatatac gttgtatcat tagacattac accagctaca ccaccaggta  
 4381 agaaaataat attagacccat ataagttcag gttctgttgggg tgctgcagca ataaacattttt

## HPV60

4441 cagatataag tgctgcagat ttaaatgtat ttgttgatcc tcagggagca ggagatagaa  
4501 taagtttgg agaagaata gagtaggcc ctattaatca gcctgctcaa ttgaaatag  
4561 aagaacctcc acgtaccagt acacctgggg agggattca acgtttaca acacgggcaa  
4621 gggattata taatagattt gtgcagcaac agccaacaca aaatattgac ttcttaggac  
4681 gtcctcccg cgctgtacaa tttgaatttgc aaaaatcccgc ctttttat gatgagggtga  
4741 ctatgcgtt tgagcaagat ttgcagagg tggctgcagc gccagaccag gattttgcag  
4801 atgtcaggga attaggacga gctcggtttt cagaaacatc tgccggaa atacgagtca  
4861 gcagatttagg aacaaaagg acaatgaaaa cacgaacttgg actaactatt ggtcggaaag  
4921 ttcaacttta ttttgcattt agtgcattt cagctgcaga aaccatcaa ctaagaacat  
4981 taggcgagtc ttcccacat ttttgcag tagataat tactgaaagt acatatatta  
5041 atttaactga aactacaat gaaggcctaa tacctgacaa tatacttagag gatgaattta  
5101 cagaaaactt taataatgca cagctgatatt ttgcacaaat agatgaagga gaatctatga  
5161 tcatgccac aattccctca ggtgtactt taaagttatt tattccgaa atagctgca  
5221 gcgtgttaaa tgggttcat ctttctctg agtggactat ttgatttgc aatgttccag  
5281 atgaaattat tcagcctgct atggcagTAG ATGtttatga tgactttat ttacatcctc  
L1 orf start ->  
first 'ATG' of L1 cds ->  
5341 atcttcttag gcgacgcaaa cggaaacggg tggattttt tAAAtgaaaa acAGATGgct  
-< L2 end /\ 3' sj  
probable L1 cds start ->  
5401 cttgggttgc agacagctgg acaattgtat cttccaccaa gcaaggctgt tgctcggtgt  
5461 ctcaatcggtt atgaatatgtt acagccaaaca aattttgtt ttcatacagg aactgacaga  
5521 atgctaattt taggacaccc ttatattgtt attatagaca gtggttcaaa taatattact  
5581 gtacctaaat gtatggaaa tcagttttaga gttatgcgcac tactattcc agatccaaac  
5641 aaatttgcacat gtatagacag agctgtctt aacccagaaaa gagagagatt agtctggaga  
5701 ttggaaaggcc ttgaaatgg tagaggtggg ctttagggaa ttggacttc tgccatcca  
5761 ttatataata aatatggaga tacagaaaaat cctggcccat atcctttaaa gcagaataat  
5821 ggtgatgaca atagaatgaa tggatggaa tggatggaa tggatggaa tggatggaa  
5881 ggtatgtaaac cagccactgg tgaacactgg gatattgcta aaccttgta tcctgctcca  
5941 gcaaaaggat cctgtcccc aattaaatca acacagtcta taattcagga cggtaatgt  
6001 tgcgatacag gcttggaaa tgcaatattt attaccttgc aagaagataa atcagggttt  
6061 cctctagata ttaccaatgaa aattttgttattt tttctgtt tactaaaaat gacaaaaat  
6121 atctatggag atgcgttattt ttctttgtt aaacgtgtt aaattttttt caggcattat  
6181 ttgttaagag gaggataga tggatgtt tggatgtt ctggatattt cttagcacca  
6241 caaactgtata aacctcaaaa taaccttgc ggttatattt actcccttac accaagtgg  
6301 tctgttagctt ctgtgtata tcaactttt aatagaccc tttttttttttt tttttttttt  
6361 ggtgcaataa atggatatttgg tgggggttac caattatttca ttactatgtt agataatact  
6421 cggaaactacta atttatcat ttcagtttac aaacaagatg ctgttttttttttttttttt  
6481 aaatataaaac aggaagattt tagacatatttttttttttttttttttttttttttttttttt  
6541 ttaattctgtt gactctgtt aatggctttt aatccatgtt ttctgttca tttaatgtt  
6601 atggacaaaaa atattttttttttttttttttttttttttttttttttttttttttttttttttt  
6661 attgaagatg cttacagata tataatgttca ctttttttttttttttttttttttttttt  
6721 aatactgaaaa gggaaagaccc ttataaacatc tatacattttt ggacaataga tttgcaagaa  
6781 cgtttttctt acgaattatc ccagtttttctt cttggaaaaaa gatatttata tcagttatggc  
6841 ttacttaacg gacaaaaacg gtctgttgc agttttgttca cgaagaaatc aaaaactgtg  
6901 aaacgtaaaaa gaactaaaTA Aatacatata tatattatattt gattaatgaa ggatattat  
-< L1 end  
6961 attaataatg ctgtgttgc aaaatgaagg attAATAAAAt tgcacatcg caagtgtctg  
signal ->  
7021 actcacgggg tctacatttt tgtctaccgc gccttcataa ttatcttggc attgcataatc  
7081 gagactataa gaaacaatca cttggcacac ttcggattt aacaagcatt gctggacact  
7141 taccaACCGT AACTGGTtaa aaaagagcgc caaagggggaa acaggcaacc gtttgcgtt  
E2 binding ->  
7201 tcctgaagga acgttttcca ggttaagtaca ttttttttttttttttttttttttttttttt  
7261 tggatggatatttgc cttttccgtt ctgtggatatttgc gcccggACC AAAAACGGTt gcc  
E2 binding ->  
//